GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:32:04 ; Search time 86.5 Seconds
(without alignments)
116.120 Million cell updates/sec

Title: US-10-608-584-1
Perfect score: 28
Sequence: 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	100.0	447	7	ADB78592	Adb78592 Human sod
2	28	100.0	1381	5	AAE20513	Aae20513 Human ion
3	28	100.0	1387	5	AAE20514	Aae20514 Human ion
4	28	100.0	1392	5	AAE20518	Aae20518 Human ion
5	28	100.0	1398	5	AAE20519	Aae20519 Human ion
6	28	100.0	1442	5	AAE20512	Aae20512 Human ion
7	28	100.0	1453	5	AAE20517	Aae20517 Human ion
8	28	100.0	1795	7	ADB78596	Adb78596 Human sod
9	28	100.0	1855	7	ADB78597	Adb78597 Human sod
10	28	100.0	1962	5	AAE20511	Aae20511 Human ion
11	28	100.0	1973	5	AAE20516	Aae20516 Human ion
12	28	100.0	1981	7	ABR83185	Abr83185 Human SCN
13	28	100.0	1998	5	AAE20510	Aae20510 Human ion
14	28	100.0	1998	7	ABR83184	Abr83184 Human SCN
15	28	100.0	1999	5	ABB06026	Abb06026 Human sod
16	28	100.0	2005	4	AAB99676	Aab99676 Human adu
17	28	100.0	2005	4	AAB99677	Aab99677 Human neo
18	28	100.0	2005	5	ABB83627	Abb83627 Human GEF
19	28	100.0	2005	7	ADB78604	Adb78604 Human sod
20	28	100.0	2005	7	ADB78603	Adb78603 Human sod
21	28	100.0	2005	7	ADB78605	Adb78605 Human sod
22	28	100.0	2005	7	ADC46947	Adc46947 Human SCN
23	28	100.0	2009	4	AAB99674	Aab99674 Human adu
24	28	100.0	2009	5	AAE20515	Aae20515 Human ion
25	28	100.0	2009	5	ABG69292	Abg69292 Human sod
26	28	100.0	2009	5	ABG69291	Abg69291 Human sod
27	28	100.0	2009	5	ABG69293	Abg69293 Human sod
28	28	100.0	2009	5	ABG69289	Abg69289 Human sod
29	28	100.0	2009	5	ABG69290	Abg69290 Human sod
30	28	100.0	2009	5	ABB83626	Abb83626 Human GEF
31	28	100.0	2009	5	AAE16776	Aae16776 Human tra
32	28	100.0	2009	7	ADB78599	Adb78599 Human sod
33	28	100.0	2009	7	ADB78595	Adb78595 Human sod
34	28	100.0	2009	7	ADB78593	Adb78593 Human sod
35	28	100.0	2009	7	ADB78594	Adb78594 Human sod
36	28	100.0	2009	7	ADB78598	Adb78598 Human sod
37	28	100.0	2009	7	ABR83180	Abr83180 Human SCN
38	28	100.0	2009	7	ADE57563	Ade57563 Human Pro
39	28	100.0	2009	7	ADE57561	Ade57561 Rat Prote
40	21	75.0	1835	2	AAR92316	Aar92316 Periphera
41	21	75.0	1977	2	AAR99641	Aar99641 Periphera
42	21	75.0	1977	8	ADE77202	Ade77202 Human pro
43	21	75.0	1977	8	ADL13028	Adl13028 Human ste
44	21	75.0	1978	7	ADE54553	Ade54553 Human Pro
45	21	75.0	1978	7	ADE54549	Ade54549 Human Pro
46	21	75.0	1984	2	AAR99639	Aar99639 Periphera
47	21	75.0	1984	7	ADE54547	Ade54547 Rat Prote
48	21	75.0	1984	7	ADE54551	Ade54551 Rat Prote
49	21	75.0	1984	7	ADE63027	Ade63027 Rat Prote
50	21	75.0	1989	2	AAR92317	Aar92317 Periphera
51	21	75.0	1989	2	AAR99640	Aar99640 Periphera
52	20	71.4	1836	7	ADE57388	Ade57388 Human Pro
53	20	71.4	1836	7	ADE59630	Ade59630 Human Pro
54	20	71.4	1836	7	ADE63029	Ade63029 Human Pro
55	20	71.4	1836	8	ADQ17412	Adq17412 Human sof
56	16	57.1	1024	5	ABB04858	Abb04858 LDL recep
57	16	57.1	1950	7	ADB78607	Adb78607 Human sod
58	16	57.1	1951	4	AAB99678	Aab99678 Human adu
59	16	57.1	1951	4	AAB99679	Aab99679 Human neo
60	16	57.1	1951	7	ADE59628	Ade59628 Rat Prote
61	16	57.1	1951	8	ADL06576	Adl06576 Human tum
62	16	57.1	1956	4	AAG65785	Aag65785 Human SNS
63	16	57.1	1956	4	AAB61996	Aab61996 Human per
64	16	57.1	1956	6	ABG76193	Abg76193 Human vol
65	16	57.1	1956	6	ABG75945	Abg75945 Human per
66	16	57.1	1956	6	ABP72253	Abp72253 Human PN3
67	16	57.1	1956	6	ADA50152	Ada50152 Human per
68	16	57.1	1956	7	ADJ68903	Adj68903 Human hea
69	16	57.1	1956	8	ADF08471	Adf08471 Human Nav
70	16	57.1	2000	5	ABB06027	Abb06027 Human sod
71	16	57.1	2000	8	ADK81762	Adk81762 Human Nav
72	15	53.6	130	5	ADK35245	Adk35245 Novel hum
73	14	50.0	1366	7	ADJ68488	Adj68488 Human hea
74	14	50.0	1366	8	ADL06575	Adl06575 Human tum
75	13	46.4	1956	4	AAG65783	Aag65783 Rat SNS1
76	13	46.4	1956	4	AAB61995	Aab61995 Rat perip
77	13	46.4	1956	6	ABG75944	Abg75944 Rat perip
78	13	46.4	1956	6	ADA50144	Ada50144 Rat perip
79	13	46.4	1956	6	ADA50153	Ada50153 Rat perip
80	13	46.4	1957	2	AAW21740	Aaw21740 Variant r
81	13	46.4	1957	2	AAW21737	Aaw21737 Wild type
82	13	46.4	1957	6	ABG76191	Abg76191 Rat volta
83	13	46.4	1957	6	ADA50156	Ada50156 Rat perip
84	13	46.4	1957	6	ADA50155	Ada50155 Rat perip
85	13	46.4	1957	7	ADD44754	Add44754 Rat Prote
86	13	46.4	1957	8	ADF08469	Adf08469 Rat Nav 1
87	13	46.4	1958	4	AAG65784	Aag65784 Mouse SNS
88	13	46.4	1962	2	AAY17250	Aay17250 NaNG poly
89	13	46.4	2132	2	AAW21739	Aaw21739 Variant r
90	12	42.9	1024	5	ABB04860	Abb04860 LDL recep
91	12	42.9	1233	4	AAB20125	Aab20125 Human sod
92	12	42.9	1243	2	AAY06598	Aay06598 Human sod
93	12	42.9	1243	4	AAB20126	Aab20126 Human sod
94	12	42.9	1444	5	AAO14926	Aao14926 Human sod
95	12	42.9	1791	4	AAB20121	Aab20121 Human sod
96	12	42.9	1791	5	AAO14925	Aao14925 Human sod
97	12	42.9	1791	7	ADD32194	Add32194 Human Na
98	11	39.3	442	4	ABG04326	Abg04326 Novel hum

99	11	39.3	1107	6	ABR41495	Abr41495 Human DIT
100	11	39.3	1603	4	AAU19518	Aau19518 Human dia

ALIGNMENTS

RESULT 1
ADB78592
ID ADB78592 standard; protein; 447 AA.
XX
AC ADB78592;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:136.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78631.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 136; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 447 AA;

Query Match 100.0%; Score 28; DB 7; Length 447;
Best Local Similarity 100.0%; Pred. No. 5.4e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426

RESULT 2
AAE20513
ID AAE20513 standard; protein; 1381 AA.
XX
AC AAE20513;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel protein #4.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW medical disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 981
FT /note= "Encoded by MTG"
FT Misc-difference 1056
FT /note= "Encoded by RCA"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025650.
XX
PR 16-AUG-2000; 2000US-0225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR N-PSDB; AAD32842.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
PS Claim 1; Page 47-50; 83pp; English.
XX
CC The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins
CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the
CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP

CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or triple helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
SQ Sequence 1381 AA;

Query Match 100.0%; Score 28; DB 5; Length 1381;
Best Local Similarity 100.0%; Pred. No. 1.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426

RESULT 3
AAE20514
ID AAE20514 standard; protein; 1387 AA.
XX
AC AAE20514;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel protein #5.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW medical disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 981
FT /note= "Encoded by MTG"
FT Misc-difference 1056
FT /note= "Encoded by RCA"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025650.
XX
PR 16-AUG-2000; 2000US-0225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR N-PSDB; AAD32843.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
PS Claim 1; Page 52-55; 83pp; English.
XX
CC The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins
CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the
CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or triple helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
SQ Sequence 1387 AA;

Query Match 100.0%; Score 28; DB 5; Length 1387;
Best Local Similarity 100.0%; Pred. No. 1.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426

RESULT 4
AAE20518
ID AAE20518 standard; protein; 1392 AA.
XX
AC AAE20518;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel protein #9.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW medical disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 992
FT /note= "Encoded by MTG"
FT Misc-difference 1067
FT /note= "Encoded by RCA"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025650.
XX
PR 16-AUG-2000; 2000US-0225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR N-PSDB; AAD32847.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
PS Claim 1; Page 75-78; 83pp; English.
XX
CC The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins

CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the
CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or triple helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
SQ Sequence 1392 AA;

Query Match 100.0%; Score 28; DB 5; Length 1392;
Best Local Similarity 100.0%; Pred. No. 1.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426

RESULT 5
AAE20519
ID AAE20519 standard; protein; 1398 AA.
XX
AC AAE20519;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel protein #10.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW medical disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 992
FT /note= "Encoded by MTG"
FT Misc-difference 1067
FT /note= "Encoded by RCA"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025650.
XX
PR 16-AUG-2000; 2000US-0225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR N-PSDB; AAD32848.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
PS Claim 1; Page 80-83; 83pp; English.
XX
CC The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins
CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the
CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or triple helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
SQ Sequence 1398 AA;

Query Match 100.0%; Score 28; DB 5; Length 1398;
Best Local Similarity 100.0%; Pred. No. 1.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426

RESULT 6
AAE20512
ID AAE20512 standard; protein; 1442 AA.
XX
AC AAE20512;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel protein #3.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW medical disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 981
FT /note= "Encoded by MTG"
FT Misc-difference 1056
FT /note= "Encoded by RCA"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025650.
XX
PR 16-AUG-2000; 2000US-0225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;

XX
DR WPI; 2002-280757/32.
DR N-PSDB; AAD32841.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
PS Claim 1; Page 43-46; 83pp; English.
XX
CC The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins
CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the
CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or triple helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
SQ Sequence 1442 AA;

Query Match 100.0%; Score 28; DB 5; Length 1442;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426

RESULT 7
AAE20517
ID AAE20517 standard; protein; 1453 AA.
XX
AC AAE20517;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel protein #8.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW medical disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 992
FT /note= "Encoded by MTG"
FT Misc-difference 1067
FT /note= "Encoded by RCA"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025650.
XX
PR 16-AUG-2000; 2000US-0225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR N-PSDB; AAD32846.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
PS Claim 1; Page 70-73; 83pp; English.
XX
CC The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins
CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the
CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or triple helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
SQ Sequence 1453 AA;

Query Match 100.0%; Score 28; DB 5; Length 1453;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426

RESULT 8
ADB78596
ID ADB78596 standard; protein; 1795 AA.
XX
AC ADB78596;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:140.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX

PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78635.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 140; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 1795 AA;

```
  Query Match             100.0%;  Score 28;  DB 7;  Length 1795;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426
```

RESULT 9
ADB78597
ID ADB78597 standard; protein; 1855 AA.
XX
AC ADB78597;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:141.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78636.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 141; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 1855 AA;

```
  Query Match             100.0%;  Score 28;  DB 7;  Length 1855;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426
```

RESULT 10
AAE20511
ID AAE20511 standard; protein; 1962 AA.

XX
AC AAE20511;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel protein #2.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW medical disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 981
FT /note= "Encoded by MTG"
FT Misc-difference 1056
FT /note= "Encoded by RCA"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025650.
XX
PR 16-AUG-2000; 2000US-0225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR N-PSDB; AAD32840.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
PS Claim 1; Page 37-41; 83pp; English.
XX
CC The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins
CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the
CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or triple helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
SQ Sequence 1962 AA;

Query Match 100.0%; Score 28; DB 5; Length 1962;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426

RESULT 11
AAE20516
ID AAE20516 standard; protein; 1973 AA.
XX
AC AAE20516;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel protein #7.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW medical disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 992
FT /note= "Encoded by MTG"
FT Misc-difference 1067
FT /note= "Encoded by RCA"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025650.
XX
PR 16-AUG-2000; 2000US-0225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR N-PSDB; AAD32845.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
PS Claim 1; Page 64-68; 83pp; English.
XX
CC The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins
CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the
CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or triple helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
SQ Sequence 1973 AA;

```
  Query Match             100.0%;  Score 28;  DB 5;  Length 1973;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426


RESULT 12
ABR83185
ID   ABR83185 standard; protein; 1981 AA.
XX
AC   ABR83185;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human SCN1A splice variant -84P:SCN1ADELp654-681.
XX
KW   SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
KW   neuroprotective; anesthetic; cytostatic; cerebroprotective; cardiant;
KW   hypotensive; gene therapy; human; splice variant.
XX
OS   Homo sapiens.
XX
PN   WO2003072751-A2.
XX
PD   04-SEP-2003.
XX
PF   25-FEB-2003; 2003WO-US006010.
XX
PR   25-FEB-2002; 2002US-0359382P.
XX
PA   (UYVA-) UNIV VANDERBILT.
XX
PI   George AL,  Lossin C;
XX
DR   WPI; 2003-712725/67.
DR   N-PSDB; ACF57880.
XX
PT   Recombinantly expressed sodium channel type 1 alpha subunit, useful in
PT   screening for modulators, for treating e.g. epilepsy.
XX
PS   Disclosure; Page 162-169; 176pp; English.
XX
CC   The invention relates to a recombinantly expressed and isolated human
CC   SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
CC   incorporated into a cell, is used to screen for specific modulators,
CC   potentially useful as anticonvulsant, antiepileptic, neuroprotective,
CC   analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
CC   epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
CC   motor endplate diseases, hypertension, congestive heart failure and
CC   muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
CC   and metastatic cancer cell lines). These activities can also be provided
CC   by gene therapy vectors that express (I) or the modulators. The
CC   modulators, also antibodies directed against (I), are used to detect
CC   sodium channel polypeptides. The present sequence represents a human
CC   SCN1A splice variant 84P:SCN1ADELp654-681
XX
SQ   Sequence 1981 AA;

  Query Match             100.0%;  Score 28;  DB 7;  Length 1981;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426


RESULT 13
AAE20510
ID   AAE20510 standard; protein; 1998 AA.
XX
AC   AAE20510;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel protein #1.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   medical disorder.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 981
FT                   /note= "Encoded by MTG"
FT   Misc-difference 1056
FT                   /note= "Encoded by RCA"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US025650.
XX
PR   16-AUG-2000; 2000US-0225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   N-PSDB; AAD32839.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders.
XX
PS   Claim 1; Page 30-34; 83pp; English.
XX
CC   The present sequence is novel human protein (NHP), ion channel protein.
CC   NHP share structural similarity with mammalian sodium channel proteins
CC   particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC   are useful as hybridisation probes for screening libraries and assessing
CC   gene expression patterns. Sequences derived from regions adjacent to the
CC   intron/exon boundaries of NHP gene can be used to design primers for use
CC   in amplification assays to detect mutations within the exons, splice
CC   sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC   nucleotide sequences are useful for drug screening effective in the
CC   treatment of symptomatic or phenotypic manifestations of perturbing the
CC   normal function of NHP in the body, and nucleotide constructs encoding
CC   NHP products are useful to genetically engineer host cells to express NHP
CC   products in vivo. These genetically engineered cells function as
CC   bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC   peptide, or a NHP fusion protein to the body. Nucleotide construct
CC   encoding NHP products are also useful in gene therapy for modulating NHP
CC   expression and to produce genetically engineered host cells to express
CC   NHP products in vivo. NHP nucleotide sequences may also be used as part
CC   of ribozyme and/or triple helix sequences that are useful for NHP gene
CC   regulation. The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases
XX
SQ   Sequence 1998 AA;

  Query Match             100.0%;  Score 28;  DB 5;  Length 1998;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
```

```
Db        399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426


RESULT 14
ABR83184
ID   ABR83184 standard; protein; 1998 AA.
XX
AC   ABR83184;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human SCN1A splice variant -33P:SCN1ADELp671-681.
XX
KW   SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
KW   neuroprotective; anesthetic; cytostatic; cerebroprotective; cardiant;
KW   hypotensive; gene therapy; human; splice variant.
XX
OS   Homo sapiens.
XX
PN   WO2003072751-A2.
XX
PD   04-SEP-2003.
XX
PF   25-FEB-2003; 2003WO-US006010.
XX
PR   25-FEB-2002; 2002US-0359382P.
XX
PA   (UYVA-) UNIV VANDERBILT.
XX
PI   George AL,  Lossin C;
XX
DR   WPI; 2003-712725/67.
DR   N-PSDB; ACF57879.
XX
PT   Recombinantly expressed sodium channel type 1 alpha subunit, useful in
PT   screening for modulators, for treating e.g. epilepsy.
XX
PS   Disclosure; Page 148-156; 176pp; English.
XX
CC   The invention relates to a recombinantly expressed and isolated human
CC   SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
CC   incorporated into a cell, is used to screen for specific modulators,
CC   potentially useful as anticonvulsant, antiepileptic, neuroprotective,
CC   analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
CC   epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
CC   motor endplate diseases, hypertension, congestive heart failure and
CC   muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
CC   and metastatic cancer cell lines). These activities can also be provided
CC   by gene therapy vectors that express (I) or the modulators. The
CC   modulators, also antibodies directed against (I), are used to detect
CC   sodium channel polypeptides. The present sequence represents a human
CC   SCN1A splice variant 33P:SCN1ADELp671-681 encoding cDNA
XX
SQ   Sequence 1998 AA;

  Query Match             100.0%;  Score 28;  DB 7;  Length 1998;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426


RESULT 15
ABB06026
ID   ABB06026 standard; protein; 1999 AA.
XX
AC   ABB06026;
XX
DT   10-MAY-2002  (first entry)
XX
DE   Human sodium channel SCN1A protein SEQ ID NO:2.
XX
KW   Human; sodium channel; SCN1A; chromosome 2q24;
KW   familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
OS   Homo sapiens.
XX
PN   WO200196552-A1.
XX
PD   20-DEC-2001.
XX
PF   12-JUN-2001; 2001WO-JP004956.
XX
PR   13-JUN-2000; 2000JP-00177540.
PR   13-JUN-2000; 2000JP-00177544.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Kanazawa I,  Goto J,  Jeong S;
XX
DR   WPI; 2002-098066/13.
DR   N-PSDB; ABL39689.
XX
PT   Human sodium channels SCN1A and SCN3A and encoded genes, useful in
PT   studying physiological mechanism in which excitant cells participate and
PT   causes of diseases and developing drugs for motor endplate disease.
XX
PS   Claim 1; Page 40-49; 88pp; Japanese.
XX
CC   The present invention describes human sodium channels SCN1A and SCN3A.
CC   The present sequence represents the human sodium channel SCN1A. SCN1A and
CC   SCN3A have been located to the human chromosome 2 long arm, positions
CC   2q24 and 2q24-31 respectively. The sodium channel proteins are useful in
CC   studying the physiological mechanism in which excitant cells participate
CC   and cause human diseases, and in developing remedies for e.g. familial
CC   hypercalcaemic periodic paralysis of extremities and motor endplate
CC   disease
XX
SQ   Sequence 1999 AA;

  Query Match             100.0%;  Score 28;  DB 5;  Length 1999;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426


RESULT 16
AAB99676
ID   AAB99676 standard; protein; 2005 AA.
XX
AC   AAB99676;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human adult form of SCN2A protein sequence SEQ ID NO:35.
XX
KW   Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW   diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW   anticonvulsant; neuroprotective.
XX
OS   Homo sapiens.
XX
PN   WO200138564-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-CA001404.
XX
PR   26-NOV-1999;   99US-0167623P.
XX
PA   (UYMC-) UNIV MCGILL.
```

XX
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR N-PSDB; AAH55793.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
PS Disclosure; Page 123-130; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 4; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428

RESULT 17
AAB99677
ID AAB99677 standard; protein; 2005 AA.
XX
AC AAB99677;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human neonatal form of SCN2A protein sequence SEQ ID NO:36.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA001404.
XX
PR 26-NOV-1999; 99US-0167623P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR N-PSDB; AAH55794.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
PS Disclosure; Page 131-138; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 4; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428

RESULT 18
ABB83627
ID ABB83627 standard; protein; 2005 AA.
XX
AC ABB83627;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human GEFS+ protein with SCN2A mutation.
XX
KW Human; GEFS+; SCN2A; mutant; mutein;
KW generalized epilepsy with febrile seizure plus.
XX
OS Homo sapiens.
XX
PN JP2002136289-A.
XX
PD 14-MAY-2002.
XX
PF 01-NOV-2000; 2000JP-00334969.
XX
PR 01-NOV-2000; 2000JP-00334969.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (RIKA) RIKAGAKU KENKYUSHO.
XX
DR WPI; 2002-552308/59.
DR N-PSDB; ABQ79201.
XX
PT A human polynucleotide which is complementary to an mRNA transcribed from
PT a generalized epilepsy with febrile seizure plus (GEFS+)-related gene
PT useful for diagnosing GEFS+.
XX
PS Claim 10; Page 29-34; 37pp; Japanese.
XX
CC This invention relates to a human polynucleotide which is complementary
CC to an mRNA transcribed from a "generalized epilepsy with febrile seizure
CC plus" (GEFS+)-related gene. The gene is useful for diagnosing GEFS+. The
CC present sequence represents the human GEFS+ protein sequence with SCN2A
CC mutation
XX
SQ Sequence 2005 AA;

```
  Query Match             100.0%;  Score 28;  DB 5;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428


RESULT 19
ADB78604
ID   ADB78604 standard; protein; 2005 AA.
XX
AC   ADB78604;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human sodium channel subunit mutant SEQ ID NO:148.
XX
KW   mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW   neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW   antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW   nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW   ion channel dysfunction; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003008574-A1.
XX
PD   30-JAN-2003.
XX
PF   08-JUL-2002; 2002WO-AU000910.
XX
PR   18-JUL-2001; 2001AU-00006452.
PR   05-MAR-2002; 2002AU-00000910.
PR   13-MAY-2002; 2002AU-00002292.
XX
PA   (BION-) BIONOMICS LTD.
PA   (WALL/) WALLACE R W.
XX
PI   Mulley JC,  Harkin LA,  Dibbens LM,  Phillips HA,  Heron SE;
PI   Berkovic SF,  Scheffer IE;
XX
DR   WPI; 2003-239332/23.
DR   N-PSDB; ADB78643.
XX
PT   Identifying predisposition to an ion channel dysfunction, such as
PT   periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT   schizophrenia, anxiety and depression, by detecting encoding-gene
PT   mutation events.
XX
PS   Claim 13; SEQ ID NO 148; 106pp; English.
XX
CC   The invention relates to a novel method for identifying a subject
CC   predisposed to a disorder associated with ion channel dysfunction. The
CC   method comprises ascertaining if at least one of the genes encoding ion
CC   channel subunits (ICS) has undergone a mutation event so that a cDNA
CC   derived from the subject has any of 134 nucleotide sequences. The method
CC   of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC   antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC   neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC   ophthalmological activity. A polynucleotide of the invention acts as an
CC   ion channel agonist, or ion channel antagonist. The methods, isolated
CC   nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC   modulator of an ion channel, cells and genetically modified non-human
CC   animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC   disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC   kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC   myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC   disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC   depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC   pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC   Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC   fibrosis, congenital stationary night blindness and total colour
CC   blindness. The present sequence represents a mutant protein of the
CC   invention. The sequence data for this patent is not represented in the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ   Sequence 2005 AA;

  Query Match             100.0%;  Score 28;  DB 7;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428


RESULT 20
ADB78603
ID   ADB78603 standard; protein; 2005 AA.
XX
AC   ADB78603;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human sodium channel subunit mutant SEQ ID NO:147.
XX
KW   mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW   neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW   antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW   nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW   ion channel dysfunction; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003008574-A1.
XX
PD   30-JAN-2003.
XX
PF   08-JUL-2002; 2002WO-AU000910.
XX
PR   18-JUL-2001; 2001AU-00006452.
PR   05-MAR-2002; 2002AU-00000910.
PR   13-MAY-2002; 2002AU-00002292.
XX
PA   (BION-) BIONOMICS LTD.
PA   (WALL/) WALLACE R W.
XX
PI   Mulley JC,  Harkin LA,  Dibbens LM,  Phillips HA,  Heron SE;
PI   Berkovic SF,  Scheffer IE;
XX
DR   WPI; 2003-239332/23.
DR   N-PSDB; ADB78642.
XX
PT   Identifying predisposition to an ion channel dysfunction, such as
PT   periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT   schizophrenia, anxiety and depression, by detecting encoding-gene
PT   mutation events.
XX
PS   Claim 13; SEQ ID NO 147; 106pp; English.
XX
CC   The invention relates to a novel method for identifying a subject
CC   predisposed to a disorder associated with ion channel dysfunction. The
CC   method comprises ascertaining if at least one of the genes encoding ion
CC   channel subunits (ICS) has undergone a mutation event so that a cDNA
CC   derived from the subject has any of 134 nucleotide sequences. The method
CC   of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC   antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC   neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC   ophthalmological activity. A polynucleotide of the invention acts as an
CC   ion channel agonist, or ion channel antagonist. The methods, isolated
```

CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 7; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428

RESULT 21
ADB78605
ID ADB78605 standard; protein; 2005 AA.
XX
AC ADB78605;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:149.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78644.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 149; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 7; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428

RESULT 22
ADC46947
ID ADC46947 standard; protein; 2005 AA.
XX
AC ADC46947;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human SCN2A amino acid sequence #SEQ ID 3.
XX
KW SCN2A; voltage-gated ion channel; human; neuroprotective; gene therapy;
KW vaccine; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO2003060525-A1.
XX
PD 24-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-EP000400.
XX
PR 17-JAN-2002; 2002EP-00001236.
PR 17-JAN-2002; 2002US-0348674P.
XX
PA (EVOT-) EVOTEC NEUROSCIENCES GMBH.
XX
PI Hipfel R, Von Der Kammer H, Pohlner J;
XX
DR WPI; 2003-598580/56.
DR N-PSDB; ADC46961.
XX
PT Diagnosing or prognosticating a neurodegenerative disease by detecting
PT the level or activity of transcription or translation products of the
PT gene coding for the voltage-gated ion channel SCN2A.
XX
PS Disclosure; Fig 9; 67pp; English.
XX

CC The invention relates to a method for diagnosing or prognosticating a
CC neurodegenerative disease in a subject, or determining whether a subject
CC is at increased risk of developing the disease. The method comprises
CC detecting the level and/or activity of a transcription or translation
CC product of the gene coding for the voltage-gated ion channel SCN2A. The
CC modulator of an activity and/or of a level of at least one substance is
CC useful for preparing a composition for treating or preventing a
CC neurodegenerative disease, in particular Alzheimer's disease. The current
CC sequence represents the human SCN2A amino acid sequence.
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 7; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428

RESULT 23
AAB99674
ID AAB99674 standard; protein; 2009 AA.
XX
AC AAB99674;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human adult form of SCN1A protein sequence SEQ ID NO:3.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA001404.
XX
PR 26-NOV-1999; 99US-0167623P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR N-PSDB; AAH55763.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
PS Disclosure; Page 96-104; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
XX
SQ Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 4; Length 2009;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426

RESULT 24
AAE20515
ID AAE20515 standard; protein; 2009 AA.
XX
AC AAE20515;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel protein #6.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW medical disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 992
FT /note= "Encoded by MTG"
FT Misc-difference 1067
FT /note= "Encoded by RCA"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025650.
XX
PR 16-AUG-2000; 2000US-0225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR N-PSDB; AAD32844.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
PS Claim 5; Page 57-62; 83pp; English.
XX
CC The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins
CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the
CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part

CC of ribozyme and/or triple helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
SQ Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 5; Length 2009;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426

RESULT 25
ABG69292
ID ABG69292 standard; protein; 2009 AA.
XX
AC ABG69292;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human sodium channel alpha 1-subunit (SCNA1) variant protein #4.
XX
KW Human; sodium channel alpha 1-subunit; SCN1A; episodic ataxia; epilepsy;
KW generalised epilepsy with febrile seizures plus; myasthenia;
KW sodium channel dysfunction; malignant hyperthermia; neuropathic pain;
KW inflammatory pain; Alzheimer's disease; Parkinson's disease; myotonia;
KW schizophrenia; hyperekplexia; anticonvulsant; analgesic; neuroprotective;
KW nootropic; anti-Parkinsonian; neuroleptic.
XX
OS Homo sapiens.
XX
PN WO200250096-A1.
XX
PD 27-JUN-2002.
XX
PF 20-DEC-2001; 2001WO-AU001648.
XX
PR 20-DEC-2000; 2000AU-00002203.
XX
PA (BION-) BIONOMICS LTD.
XX
PI Wallace RH, Mulley JC, Berkovic SF;
XX
DR WPI; 2002-528445/56.
XX
PT New nucleic acid encoding mutant alpha subunit of a mammalian voltage-
PT gated sodium channel, useful for diagnosis of epilepsy, particularly
PT generalized epilepsy with febrile seizures plus.
XX
PS Claim 53; Page 147-157; 198pp; English.
XX
CC The invention relates to a nucleic acid molecule encoding a mutant alpha
CC subunit of a mammalian voltage-gated sodium channel. The DNA and the
CC polypeptide may be used in the diagnosis of epilepsy, in particular
CC generalised epilepsy with febrile seizures plus, and other disorders
CC associated with sodium channel dysfunction. The polypeptide is useful for
CC the screening of candidate pharmaceutical agents, where high throughput
CC screening techniques are employed. The sequences are also useful in the
CC manufacture of a medicament for the treatment of a disorder associated
CC with sodium channel dysfunction such as epilepsy, particularly
CC generalised epilepsy with febrile seizures plus, malignant hyperthermia,
CC myasthenia, episodic ataxia, neuropathic and inflammatory pain,
CC Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia
CC and myotonias. Sequences ABG69289-ABG69293 represent human sodium channel
CC alpha 1-subunit (SCN1A) polypeptides of the invention
XX
SQ Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 5; Length 2009;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426

Search completed: January 27, 2005, 17:45:13
Job time : 90.5 secs

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:36:05 ; Search time 17 Seconds
(without alignments)
158.475 Million cell updates/sec

Title: US-10-608-584-1
Perfect score: 28
Sequence: 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	100.0	2005	2	A46269	sodium channel alp
2	28	100.0	2005	2	B25019	sodium channel pro
3	28	100.0	2009	2	A25019	sodium channel pro
4	21	75.0	1820	1	CHEE	sodium channel pro
5	21	75.0	1977	2	S54771	sodium channel alp
6	21	75.0	2049	2	T43161	sodium channel pro
7	20	71.4	1835	2	I54323	sodium channel alp
8	20	71.4	1836	2	I64893	sodium channel alp
9	20	71.4	1836	2	JS0648	sodium channel alp
10	20	71.4	1836	2	I51964	sodium channel alp
11	20	71.4	1840	1	CHRTM1	sodium channel pro
12	16	57.1	1951	2	S00320	sodium channel pro
13	16	57.1	1983	2	A60054	sodium channel pro
14	13	46.4	1957	2	S68453	sodium channel pro
15	11	39.3	1976	2	I56555	sodium channel pro
16	11	39.3	2016	2	A38195	sodium channel pro
17	11	39.3	2019	2	A33996	sodium channel pro
18	10	35.7	1784	2	T43167	sodium channel pro
19	9	32.1	286	2	S16294	chlorophyll a/b-bi
20	9	32.1	286	2	S21386	chlorophyll a/b-bi
21	9	32.1	1765	2	T42388	sodium channel alp
22	8	28.6	103	2	A53461	voltage-sensitive
23	8	28.6	245	2	T15794	hypothetical prote
24	8	28.6	575	2	D69611	ABC transporter re
25	8	28.6	1034	2	S60051	sodium channel alp
26	8	28.6	1034	2	S60060	sodium channel alp
27	8	28.6	1321	2	A60165	sodium channel pro
28	8	28.6	1689	2	S72467	sodium channel pro
29	8	28.6	1820	2	A33299	sodium channel pro
30	8	28.6	2108	2	S72458	sodium channel pro
31	7	25.0	211	2	F70029	conserved hypothet
32	7	25.0	308	2	JC2253	chitinase (EC 3.2.
33	7	25.0	318	2	S14948	chitinase (EC 3.2.
34	7	25.0	349	2	A72605	probable high-affi
35	7	25.0	361	2	T33402	hypothetical prote
36	7	25.0	365	1	S77076	phospho-N-acetylmu
37	7	25.0	376	2	A36978	MAP kinase mpk-1 (
38	7	25.0	444	2	A36977	MAP kinase sur-1 (
39	7	25.0	724	2	B85045	probable calcium c
40	7	25.0	800	2	T26683	hypothetical prote
41	7	25.0	844	2	E69000	cation-transportin
42	7	25.0	1217	2	C86159	hypothetical prote
43	6	21.4	50	2	D91083	hypothetical prote
44	6	21.4	51	2	I61238	heparin-binding ep
45	6	21.4	59	2	S56139	membrane protein n
46	6	21.4	72	2	AH0039	probable exported
47	6	21.4	82	2	B43702	X'82 protein - Afr
48	6	21.4	84	2	S27162	heparin-binding ep
49	6	21.4	103	1	BVYCGS	chaperonin groES -
50	6	21.4	103	2	A36721	groES protein - Sy
51	6	21.4	106	2	D69931	hypothetical prote
52	6	21.4	106	2	T22069	hypothetical prote
53	6	21.4	115	2	T17085	NADH2 dehydrogenas
54	6	21.4	118	2	I45348	V118 protein - Afr
55	6	21.4	121	2	A36821	LIS121-1 protein -
56	6	21.4	124	2	B36821	LIS124-2 protein -
57	6	21.4	124	2	C36821	LIS124-1 protein -
58	6	21.4	124	2	C43702	U124 protein - Afr
59	6	21.4	135	2	T05909	membrane protein Y
60	6	21.4	141	2	A86417	probable auxin-ind
61	6	21.4	157	2	D83742	cytochrome c oxida
62	6	21.4	159	2	B70635	hypothetical prote
63	6	21.4	166	2	D70553	hypothetical prote
64	6	21.4	181	2	B84121	hypothetical prote
65	6	21.4	189	2	T02423	probable low tempe
66	6	21.4	197	2	T07995	ycf4 protein - Chl
67	6	21.4	201	2	G72663	hypothetical prote
68	6	21.4	201	2	G90385	hypothetical prote
69	6	21.4	208	1	A38432	heparin-binding EG
70	6	21.4	208	1	A41914	diptheria toxin re
71	6	21.4	213	2	A75218	hypothetical prote
72	6	21.4	215	2	I38473	olfactory receptor
73	6	21.4	218	2	G95016	conserved hypothet
74	6	21.4	227	2	B81054	dedA protein, prob
75	6	21.4	227	2	B70790	hypothetical prote
76	6	21.4	234	2	A70131	phosphatidyltransf
77	6	21.4	238	2	T33550	hypothetical prote
78	6	21.4	240	2	H97783	hypothetical prote
79	6	21.4	246	2	S15378	H+-transporting tw
80	6	21.4	247	2	T11315	ATP synthase chain
81	6	21.4	249	2	T27019	hypothetical prote
82	6	21.4	252	2	B98204	probable permease
83	6	21.4	252	2	AF3082	hypothetical prote
84	6	21.4	254	1	G69878	conserved hypothet
85	6	21.4	259	2	B83419	conserved hypothet
86	6	21.4	261	2	B81823	DedA-family integr
87	6	21.4	261	2	B90107	putative CCR4-asso
88	6	21.4	266	2	C87367	flagellar biosynth
89	6	21.4	273	2	T37841	probable transloca
90	6	21.4	273	2	AI1864	hypothetical prote
91	6	21.4	276	2	A72276	phosphate ABC tran
92	6	21.4	279	2	D89784	hypothetical prote
93	6	21.4	280	2	D84015	maltose/maltodextr
94	6	21.4	282	2	AI0948	hypothetical prote
95	6	21.4	283	2	E83902	maltose/maltodextr
96	6	21.4	284	2	AC2551	hypothetical prote
97	6	21.4	284	2	E97054	sporulation protei
98	6	21.4	288	2	T37395	probable 33.6K pro
99	6	21.4	288	2	A42518	A8R protein - vacc
100	6	21.4	288	2	F72164	A9R protein - vari

ALIGNMENTS

RESULT 1
A46269
sodium channel alpha chain HBA - human
C;Species: Homo sapiens (man)
C;Date: 20-Oct-1993 #sequence_revision 18-Nov-1994 #text_change 21-Nov-1997
C;Accession: A46269
R;Ahmed, C.M.; Ware, D.H.; Lee, S.C.; Patten, C.D.; Ferrer-Montiel, A.V.; Schinder, A.F.
Proc. Natl. Acad. Sci. U.S.A. 89, 8220-8224, 1992
A;Title: Primary structure, chromosomal localization, and functional expression of a vol
A;Reference number: A46269; MUID:92390418; PMID:1325650
A;Accession: A46269
A;Molecule type: mRNA
A;Residues: 1-2005 <AHM>
A;Cross-references: GB:M94055
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:113082)
C;Genetics:
A;Map position: 2q23-q24.3
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 100.0%; Score 28; DB 2; Length 2005;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428

RESULT 2
B25019
sodium channel protein II - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: B25019; S24804
R;Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H
Nature 320, 188-192, 1986
A;Title: Existence of distinct sodium channel messenger RNAs in rat brain.
A;Reference number: A93377; MUID:86146901; PMID:3754035
A;Accession: B25019
A;Molecule type: mRNA
A;Residues: 1-2005 <NOD>
A;Cross-references: UNIPROT:Q63509
A;Experimental source: brain
R;Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
submitted to the EMBL Data Library, August 1991
A;Description: Developmentally regulated RNA splicing of rat brain sodium channel mRNAs.
A;Reference number: S24803
A;Accession: S24804
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 183-188,'D',190-305 <SAR>
A;Cross-references: EMBL:X61149; NID:g57074; PIDN:CAA43458.1; PID:g57076
C;Superfamily: sodium channel protein
C;Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-g

Query Match 100.0%; Score 28; DB 2; Length 2005;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428

RESULT 3
A25019
sodium channel protein I - rat
N;Alternate names: sodium channel protein A
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A25019; S40783; I84764
R;Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi,
Nature 320, 188-192, 1986
A;Title: Existence of distinct sodium channel messenger RNAs in rat brain.
A;Reference number: A93377; MUID:86146901; PMID:3754035
A;Accession: A25019
A;Molecule type: mRNA
A;Residues: 1-2009 <NOD>
A;Cross-references: UNIPROT:P04774; GB:X03638; NID:g57216; PIDN:CAA27286.1; PID:g57217
A;Experimental source: brain
R;Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
Nucleic Acids Res. 19, 5673-5679, 1991
A;Title: Developmentally regulated alternative RNA splicing of rat brain sodium channe
A;Reference number: S40782; MUID:92051314; PMID:1658739
A;Accession: S40783
A;Molecule type: DNA
A;Residues: 177-253 <SAR>
R;Noda, M.; Numa, S.
J. Recept. Res. 7, 467-497, 1987
A;Title: Structure and function of sodium channel.
A;Reference number: I50536; MUID:87311395; PMID:2442385
A;Accession: I84764
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2009 <RES>
A;Cross-references: GB:M22253; NID:g1041088; PIDN:AAA79965.1; PID:g1041089
C;Superfamily: sodium channel protein
C;Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-

Query Match 100.0%; Score 28; DB 2; Length 2009;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||||||||
Db 399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426

RESULT 4
CHEE
sodium channel protein - electric eel
C;Species: Electrophorus electricus (electric eel)
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03178; I50536
R;Noda, M.; Shimizu, S.; Tanabe, T.; Takai, T.; Kayano, T.; Ikeda, T.; Takahashi, H.; N
da, H.; Miyata, T.; Numa, S.
Nature 312, 121-127, 1984
A;Title: Primary structure of Electrophorus electricus sodium channel deduced from cDNA
A;Reference number: A03178; MUID:85061498; PMID:6209577
A;Accession: A03178
A;Molecule type: mRNA
A;Residues: 1-1820 <NOD>
A;Cross-references: UNIPROT:P02719; GB:X01119; NID:g62776; PIDN:CAA25587.1; PID:g62777
R;Noda, M.; Numa, S.
J. Recept. Res. 7, 467-497, 1987
A;Title: Structure and function of sodium channel.
A;Reference number: I50536; MUID:87311395; PMID:2442385
A;Accession: I50536
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1820 <NO2>
A;Cross-references: GB:M22252; NID:g1041048; PIDN:AAA79960.1; PID:g1041049
C;Comment: This membrane glycoprotein mediates the voltage-dependent sodium-ion permeabi
ss the membrane, the protein forms a sodium-selective channel through which sodium ions
C;Comment: This sequence contains four highly homologous internal repeats (excluding ree
Each repeat has a similar overall structure containing six subregions located in identi
has a net positive charge (S4), and one is neutral (S2).
C;Comment: The four repeating units are thought to be oriented pseudosymmetrically acros
e. The presence of four homologous structures within this molecule is consistent with th
C;Comment: Available data suggest that activation and inactivation gates are located nea
955 might, in conjunction with the positively charged residues of S4, act as a voltage s

C;Superfamily: sodium channel protein
C;Keywords: duplication; glycoprotein; ion transport; membrane protein; sodium channel;
F;111-419,555-807,989-1281,1311-1587/Region: duplication internal repeats I, II, III and
F;111-141,555-585,989-1019,1311-1341/Region: S1 of repeats I through IV
F;150-171,597-620,1033-1057,1353-1376/Region: S2 of repeats I through IV
F;177-197,626-643,1062-1079,1381-1398/Region: S3 of repeats I through IV
F;204-224,651-671,1092-1112,1417-1437/Region: S4 of repeats I through IV
F;244-264,691-711,1132-1152,1454-1474/Region: S5 of repeats I through IV
F;379-402,767-790,1236-1264,1544-1567/Region: S6 of repeats I through IV
F;205,278,288,317,591,690,797,1160,1174,1806/Binding site: carbohydrate (Asn) (covalent)

Query Match 75.0%; Score 21; DB 1; Length 1820;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||
Db 385 VIFLGSFYLINLILAVVAMAY 405

RESULT 5
S54771
sodium channel alpha subunit - human
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54771
R;Klugbauer, N.; Lacinova, L.; Flockerzi, V.; Hofmann, F.
EMBO J. 14, 1084-1090, 1995
A;Title: Structure and functional expression of a new member of the tetrodotoxin-sensiti
A;Reference number: S54771; MUID:95237189; PMID:7720699
A;Accession: S54771
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1977 <KLU>
A;Cross-references: UNIPROT:Q15858; EMBL:X82835; NID:g758109; PIDN:CAA58042.1; PID:g7581
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 75.0%; Score 21; DB 2; Length 1977;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||
Db 385 VIFLGSFYLINLILAVVAMAY 405

RESULT 6
T43161
sodium channel protein TuNaI - sea squirt (Halocynthia roretzi)
C;Species: Halocynthia roretzi
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43161
R;Okamura, Y.; Ono, F.; Okagaki, R.; Chong, J.; Mandel, G.
Neuron 13, 937-948, 1994
A;Title: Neural expression of a sodium channel gene requires cell-specific interactions.
A;Reference number: Z22320; MUID:95033215; PMID:7946338
A;Accession: T43161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2049 <OKA>
A;Cross-references: UNIPROT:Q25150; EMBL:D17311; PIDN:BAA04133.1
C;Superfamily: sodium channel protein
C;Keywords: sodium channel; transmembrane protein

Query Match 75.0%; Score 21; DB 2; Length 2049;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VIFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||||
Db 449 VIFLGSFYLINLILAVVAMAY 469

RESULT 7
I54323
sodium channel alpha subunit - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C;Accession: I54323
R;McClatchey, A.I.; Lin, C.S.; Wang, J.; Hoffman, E.P.; Rojas, C.; Gusella, J.F.
Hum. Mol. Genet. 1, 521-527, 1992
A;Title: The genomic structure of the human skeletal muscle sodium channel gene.
A;Reference number: I54323; MUID:93338444; PMID:1339144
A;Accession: I54323
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1835 <RES>
A;Cross-references: GB:L01983; NID:g337992; PIDN:AAA75557.1; PID:g908809
C;Genetics:
A;Gene: GDB:SCN4A
A;Cross-references: GDB:125181; OMIM:170500
A;Map position: 17q23.1-17q25.3
A;Introns: 91/3; 131/2; 161/2; 204/2; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/3;
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 71.4%; Score 20; DB 2; Length 1835;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||
Db 431 IFLGSFYLINLILAVVAMAY 450

RESULT 8
I64893
sodium channel alpha subunit - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: I64893
R;George, A.L.
Ann. Neurol. 31, 131-137, 1992
A;Title: Primary structure of the adult human skeletal muscle voltage-dependent sodium
A;Reference number: I51964; MUID:92246457; PMID:1315496
A;Accession: I64893
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1836 <RES>
A;Cross-references: UNIPROT:P35499; GB:M81758; NID:g338212; PIDN:AAA60554.1; PID:g33821
C;Genetics:
A;Gene: SkM1
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 71.4%; Score 20; DB 2; Length 1836;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IFLGSFYLINLILAVVAMAY 28
||||||||||||||||||||
Db 431 IFLGSFYLINLILAVVAMAY 450

RESULT 9
JS0648
sodium channel alpha chain - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JS0648; A42099
R;Wang, J.; Rojas, C.V.; Zhou, J.; Schwartz, L.S.; Nicholas, H.; Hoffmann, E.P.
Biochem. Biophys. Res. Commun. 182, 794-801, 1992
A;Title: Sequence and genomic structure of the human adult skeletal muscle sodium channe
A;Reference number: JS0648; MUID:92134303; PMID:1310396
A;Accession: JS0648

A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1836 <WAN>
A;Cross-references: UNIPROT:P35499
A;Note: 861-Asp was also found as the result of polymorphism
R;McClatchey, A.I.; Van den Bergh, P.; Pericak-Vance, M.A.; Raskind, W.; Verellen, C.; M
Cell 68, 769-774, 1992
A;Title: Temperature-sensitive mutations in the III-IV cytoplasmic loop region of the sk
A;Reference number: A42099; MUID:92154689; PMID:1310898
A;Accession: A42099
A;Molecule type: DNA
A;Residues: 1299-1351 <MCC>
A;Cross-references: GB:S82622; NID:g245611; PIDN:AAB21450.1; PID:g245612
A;Experimental source: skeletal muscle
A;Note: sequence extracted from NCBI backbone (NCBIN:82622, NCBIP:82623)
C;Genetics:
A;Gene: GDB:SCN4A
A;Cross-references: GDB:125181; OMIM:170500
A;Map position: 17q23.1-17q25.3
C;Superfamily: sodium channel protein
C;Keywords: duplication; glycoprotein; phosphoprotein; transmembrane protein
F;129-150/Domain: transmembrane #status predicted <TR1>
F;159-178/Domain: transmembrane #status predicted <TR2>
F;191-210/Domain: transmembrane #status predicted <TR3>
F;217-236/Domain: transmembrane #status predicted <TR4>
F;253-266/Domain: transmembrane #status predicted <TR5>
F;424-449/Domain: transmembrane #status predicted <TR6>
F;574-597/Domain: transmembrane #status predicted <RI1>
F;609-632/Domain: transmembrane #status predicted <RI2>
F;641-660/Domain: transmembrane #status predicted <RI3>
F;667-686/Domain: transmembrane #status predicted <RI4>
F;702-724/Domain: transmembrane #status predicted <RI5>
F;777-802/Domain: transmembrane #status predicted <RI6>
F;1027-1049/Domain: transmembrane #status predicted <II1>
F;1064-1089/Domain: transmembrane #status predicted <II2>
F;1096-1116/Domain: transmembrane #status predicted <II3>
F;1122-1143/Domain: transmembrane #status predicted <II4>
F;1163-1184/Domain: transmembrane #status predicted <II5>
F;1269-1295/Domain: transmembrane #status predicted <II6>
F;1349-1372/Domain: transmembrane #status predicted <VS1>
F;1384-1407/Domain: transmembrane #status predicted <VS2>
F;1414-1437/Domain: transmembrane #status predicted <VS3>
F;1447-1469/Domain: transmembrane #status predicted <VS4>
F;1485-1507/Domain: transmembrane #status predicted <VS5>
F;1574-1598/Domain: transmembrane #status predicted <VS6>
F;21,149,220,378,415,1019,1130,1242,1313,1721,1826/Binding site: phosphate (Thr) (covale
F;56,251,513,653,1511,1746/Binding site: phosphate (Ser) (covalent) (by protein kinase A
F;214,288,291,297,303,315,321,333,362,507,702,961,1191,1205/Binding site: carbohydrate (
F;246,670,725,850,950,1127,1195,1328/Binding site: phosphate (Ser) (covalent) (by protei
F;387,457/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predict

Query Match 71.4%; Score 20; DB 2; Length 1836;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          9 IFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||
Db        431 IFLGSFYLINLILAVVAMAY 450
```

RESULT 10
I51964
sodium channel alpha chain SCN4A, skeletal muscle - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I51964
R;George, A.L.
Ann. Neurol. 31, 131-137, 1992
A;Title: Primary structure of the adult human skeletal muscle voltage-dependent sodium c
A;Reference number: I51964; MUID:92246457; PMID:1315496
A;Accession: I51964
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1836 <RES>
A;Cross-references: UNIPROT:P35499; GB:L04236; NID:g292485; PIDN:AAB59624.1; PID:g292487
C;Genetics:
A;Gene: GDB:SCN4A
A;Cross-references: GDB:125181; OMIM:170500
A;Map position: 17q23.1-17q25.3
A;Introns: 91/3; 131/2; 161/2; 204/2; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/3;
C;Superfamily: sodium channel protein
C;Keywords: duplication; skeletal muscle

Query Match 71.4%; Score 20; DB 2; Length 1836;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          9 IFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||
Db        431 IFLGSFYLINLILAVVAMAY 450
```

RESULT 11
CHRTM1
sodium channel protein mu1 alpha chain, skeletal muscle - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: JN0007
R;Trimmer, J.S.; Cooperman, S.S.; Tomiko, S.A.; Zhou, J.; Crean, S.M.; Boyle, M.B.; Kall
Neuron 3, 33-49, 1989
A;Title: Primary structure and functional expression of a mammalian skeletal muscle sodi
A;Reference number: JN0007; MUID:90148778; PMID:2559760
A;Accession: JN0007
A;Molecule type: mRNA
A;Residues: 1-1840 <TRI>
A;Cross-references: UNIPROT:P15390; GB:M26643; NID:g205651; PIDN:AAA41682.1; PID:g205652
C;Comment: Action potentials propagated by skeletal muscle sodium channels are responsib
C;Comment: This heavily glycosylated protein contains four homologous domains, each of w
C;Comment: This protein is distinct from but related to sodium channel proteins isolated
C;Superfamily: sodium channel protein
C;Keywords: duplication; glycoprotein; ion transport; neuromuscular junction; phosphopro
F;120-458,561-813,1013-1305,1335-1611/Region: duplication
F;56,251,1321,1504/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #
F;214,288,291,297,303,309,315,327,356,502,696,954,1184,1198,1563,1702/Binding site: carb

Query Match 71.4%; Score 20; DB 1; Length 1840;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          9 IFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||
Db        425 IFLGSFYLINLILAVVAMAY 444
```

RESULT 12
S00320
sodium channel protein III - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S00320
R;Kayano, T.; Noda, M.; Flockerzi, V.; Takahashi, H.; Numa, S.
FEBS Lett. 228, 187-194, 1988
A;Title: Primary structure of rat brain sodium channel III deduced from the cDNA sequenc
A;Reference number: S00320; MUID:88137594; PMID:2449363
A;Accession: S00320
A;Molecule type: mRNA
A;Residues: 1-1951 <KAY>
A;Cross-references: UNIPROT:P08104; EMBL:Y00766; NID:g57210; PIDN:CAA68735.1; PID:g57211
A;Note: 270-Ile, 278-Leu, 355-Thr, 513-Lys, and 1059-Arg were also found
C;Superfamily: sodium channel protein
C;Keywords: duplication; transmembrane protein

Query Match 57.1%; Score 16; DB 2; Length 1951;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 YMIFFVLVIFLGSFYL 16
              ||||||||||||||||
Db        400 YMIFFVLVIFLGSFYL 415


RESULT 13
A60054
sodium channel protein IIIb, long form - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60054; B44824
R;Joho, R.H.; Moorman, J.R.; VanDongen, A.M.J.; Kirsch, G.E.; Silberberg, H.; Schuster,
Brain Res. Mol. Brain Res. 7, 105-113, 1990
A;Title: Toxin and kinetic profile of rat brain type III sodium channels expressed in Xe
A;Reference number: A60054; MUID:90251117; PMID:2160038
A;Accession: A60054
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1983 <JOH>
A;Cross-references: UNIPROT:Q64243
R;Schaller, K.L.; Krzemien, D.M.; McKenna, N.M.; Caldwell, J.H.
J. Neurosci. 12, 1370-1381, 1992
A;Title: Alternatively spliced sodium channel transcripts in brain and muscle.
A;Reference number: A44824; MUID:92211397; PMID:1313493
A;Accession: B44824
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 611-662 <SCH>
A;Cross-references: GB:S97388; NID:g248225; PIDN:AAB21984.1; PID:g248226
A;Experimental source: skeletal muscle
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:97388, NCBIP:97391)
C;Superfamily: sodium channel protein
C;Keywords: duplication; glycoprotein; ion transport; sodium channel; transmembrane prot

  Query Match             57.1%;  Score 16;  DB 2;  Length 1983;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYL 16
              ||||||||||||||||
Db        400 YMIFFVLVIFLGSFYL 415


RESULT 14
S68453
sodium channel protein SNS - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: S68453
R;Akopian, A.N.; Sivilotti, L.; Wood, J.N.
Nature 379, 257-262, 1996
A;Title: A tetrodotoxin-resistant voltage-gated sodium channel expressed by sensory neur
A;Reference number: S68453; MUID:96138382; PMID:8538791
A;Accession: S68453
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1957 <AKO>
A;Cross-references: UNIPROT:Q63554; GB:X92184; NID:g1209466; PIDN:CAA63095.1; PID:g12094
A;Experimental source: dorsal root ganglia
C;Superfamily: sodium channel protein
C;Keywords: sodium channel; transmembrane protein; voltage-gated ion channel
F;132-148/Domain: transmembrane #status predicted <TM1>
F;158-174/Domain: transmembrane #status predicted <TM2>
F;225-241/Domain: transmembrane #status predicted <TM3>
F;249-265/Domain: transmembrane #status predicted <TM4>
F;376-392/Domain: transmembrane #status predicted <TM5>
F;666-682/Domain: transmembrane #status predicted <TM6>
F;702-718/Domain: transmembrane #status predicted <TM7>
F;731-747/Domain: transmembrane #status predicted <TM8>
F;788-804/Domain: transmembrane #status predicted <TM9>
F;865-881/Domain: transmembrane #status predicted <TM10>
F;1156-1172/Domain: transmembrane #status predicted <TM11>
F;1194-1210/Domain: transmembrane #status predicted <TM12>
F;1221-1237/Domain: transmembrane #status predicted <TM13>
F;1286-1302/Domain: transmembrane #status predicted <TM14>
F;1400-1416/Domain: transmembrane #status predicted <TM15>
F;1482-1498/Domain: transmembrane #status predicted <TM16>
F;1516-1532/Domain: transmembrane #status predicted <TM17>
F;1546-1562/Domain: transmembrane #status predicted <TM18>
F;1606-1622/Domain: transmembrane #status predicted <TM19>
F;1708-1724/Domain: transmembrane #status predicted <TM20>

  Query Match             46.4%;  Score 13;  DB 2;  Length 1957;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 FFVLVIFLGSFYL 16
              |||||||||||||
Db        375 FFVLVIFLGSFYL 387


RESULT 15
I56555
sodium channel protein 6 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56555
R;Schaller, K.L.; Krzemien, D.M.; Yarowsky, P.J.; Krueger, B.K.; Caldwell, J.H.
J. Neurosci. 15, 3231-3242, 1995
A;Title: A novel, abundant sodium channel expressed in neurons and glia.
A;Reference number: I56555; MUID:95271284; PMID:7751906
A;Accession: I56555
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1976 <RES>
A;Cross-references: UNIPROT:Q63541; GB:L39018; NID:g829033; PIDN:AAC42059.1; PID:g82903
C;Genetics:
A;Gene: SCP6
C;Superfamily: sodium channel protein
C;Keywords: duplication

  Query Match             39.3%;  Score 11;  DB 2;  Length 1976;
  Best Local Similarity   100.0%;  Pred. No. 0.0086;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 NLILAVVAMAY 28
              ||||||||||
Db        405 NLILAVVAMAY 415


RESULT 16
A38195
sodium channel protein hHI, cardiac - human
N;Alternate names: tetrodotoxin-insensitive, voltage-dependent sodium channel, TTX-I Na
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A38195
R;Gellens, M.E.; George Jr., A.L.; Chen, L.Q.; Chahine, M.; Horn, R.; Barchi, R.L.; Kal
Proc. Natl. Acad. Sci. U.S.A. 89, 554-558, 1992
A;Title: Primary structure and functional expression of the human cardiac tetrodotoxin-
A;Reference number: A38195; MUID:92115699; PMID:1309946
A;Accession: A38195
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-2016 <GEL>
A;Cross-references: UNIPROT:Q14524; GB:M77235; NID:g184038; PIDN:AAA58644.1; PID:g184039
A;Experimental source: heart
C;Superfamily: sodium channel protein
C;Keywords: cardiac muscle; duplication; glycoprotein; heart; ion transport; sodium char

  Query Match             39.3%;  Score 11;  DB 2;  Length 2016;
  Best Local Similarity   100.0%;  Pred. No. 0.0087;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 NLILAVVAMAY 28
```

```
                ||||||||||||
Db        406 NLILAVVAMAY 416


RESULT 17
A33996
sodium channel protein I, cardiac - rat
N;Alternate names: sodium channel protein (SkM2) alpha chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33996; JQ0412
R;Rogart, R.B.; Cribbs, L.L.; Muglia, L.K.; Kephart, D.D.; Kaiser, M.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 8170-8174, 1989
A;Title: Molecular cloning of a putative tetrodotoxin-resistant rat heart Na(+) channel
A;Reference number: A33996; MUID:90046760; PMID:2554302
A;Accession: A33996
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2019 <ROG>
A;Cross-references: UNIPROT:P15389; GB:M27902; NID:g206857; PIDN:AAA42114.1; PID:g206858
R;Kallen, R.G.; Sheng, Z.H.; Yang, J.; Chen, L.; Rogart, R.B.; Barchi, R.L.
Neuron 4, 233-242, 1990
A;Title: Primary structure and expression of a sodium channel characteristic of denervat
A;Reference number: JQ0412; MUID:90166613; PMID:2155010
A;Accession: JQ0412
A;Molecule type: mRNA
A;Residues: 1-479,481-1712,'T',1714-1963,'R',1965-2019 <KAL>
A;Experimental source: muscle
C;Superfamily: sodium channel protein
C;Keywords: cardiac muscle; duplication; heart; sodium channel; transmembrane protein

  Query Match             39.3%;  Score 11;  DB 2;  Length 2019;
  Best Local Similarity   100.0%;  Pred. No. 0.0087;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 NLILAVVAMAY 28
              ||||||||||||
Db        407 NLILAVVAMAY 417


RESULT 18
T43167
sodium channel protein - California market squid
C;Species: Loligo opalescens (California market squid)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43167
R;Rosenthal, J.J.; Gilly, W.F.
Proc. Natl. Acad. Sci. U.S.A. 90, 10026-10030, 1993
A;Title: Amino acid sequence of a putative sodium channel expressed in the giant axon of
A;Reference number: Z22324; MUID:94052096; PMID:8234251
A;Accession: T43167
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1784 <ROS>
A;Cross-references: UNIPROT:Q25377; EMBL:L19979; NID:g349118; PID:g349119; PIDN:AAA16202
A;Experimental source: stellate ganglia
C;Superfamily: sodium channel protein
C;Keywords: ion transport; membrane protein; sodium channel; voltage-gated ion channel

  Query Match             35.7%;  Score 10;  DB 2;  Length 1784;
  Best Local Similarity   100.0%;  Pred. No. 0.074;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 LVIFLGSFYL 16
              ||||||||||
Db        383 LVIFLGSFYL 392


RESULT 19
S16294
chlorophyll a/b-binding protein type I precursor - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S16294
R;Pichersky, E.; Subramaniam, R.; White, M.J.; Reid, J.; Aebersold, R.; Green, B.R.
Mol. Gen. Genet. 227, 277-284, 1991
A;Title: Chlorophyll a/b binding (CAB) polypeptides of CP29, the internal chlorophyll a
or a second CP29 polypeptide.
A;Reference number: S16294; MUID:91287707; PMID:2062308
A;Accession: S16294
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <GRE>
A;Cross-references: UNIPROT:Q00321
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: chloroplast; thylakoid

  Query Match             32.1%;  Score 9;  DB 2;  Length 286;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 INLILAVVA 25
              |||||||||
Db        175 INLILAVVA 183


RESULT 20
S21386
chlorophyll a/b-binding protein CP29 precursor - barley
C;Species: Hordeum vulgare (barley)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S21386
R;Sorensen, A.B.; Jensen, B.F.; Gausing, K.
submitted to the EMBL Data Library, October 1991
A;Description: Barley (Hordeum vulgare) gene for CP29, a core chlorophyll a/b binding pr
A;Reference number: S21386
A;Accession: S21386
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <SOR>
A;Cross-references: UNIPROT:Q40039; EMBL:X63052; NID:g18957; PIDN:CAA44777.1; PID:g18958
C;Genetics:
A;Introns: 70/1; 98/2; 115/2; 155/3; 200/3
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: chloroplast; thylakoid

  Query Match             32.1%;  Score 9;  DB 2;  Length 286;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 INLILAVVA 25
              |||||||||
Db        175 INLILAVVA 183


RESULT 21
T42388
sodium channel alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42388
R;Dib-Hajj, S.D.; Tyrrell, L.; Black, J.A.; Waxman, S.G.
Proc. Natl. Acad. Sci. U.S.A. 95, 8963-8968, 1998
A;Title: NaN, a novel voltage-gated Na channel, is expressed preferentially in periphera
A;Reference number: Z22149; MUID:98338024; PMID:9671787
A;Accession: T42388
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1765 <DIB>
A;Cross-references: UNIPROT:O88457; EMBL:AF059030; NID:g3372614; PID:g3372615; PIDN:AAC4
A;Experimental source: strain Sprague-Dawley; dorsal root ganglia
A;Note: preferentially expressed in sensory neurons within dorsal root ganglia and trige
C;Superfamily: sodium channel protein

  Query Match             32.1%;  Score 9;  DB 2;  Length 1765;
  Best Local Similarity   100.0%;  Pred. No. 0.69;
```

```
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYL 16
              |||||||||
Db        378 VIFLGSFYL 386


RESULT 22
A53461
voltage-sensitive sodium channel - house fly (fragment)
C;Species: Musca domestica (house fly)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A53461
R;Knipple, D.C.; Doyle, K.E.; Marsella-Herrick, P.A.; Soderlund, D.M.
Proc. Natl. Acad. Sci. U.S.A. 91, 2483-2487, 1994
A;Title: Tight genetic linkage between the kdr insecticide resistance trait and a voltag
A;Reference number: A53461; MUID:94195766; PMID:8146143
A;Contents: NAIDM, insecticide-susceptible
A;Accession: A53461
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-103 <KNI>
A;Cross-references: UNIPROT:Q25439; UNIPROT:Q25440; UNIPROT:Q94615
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:146081, NCBIP:146080)
C;Superfamily: sodium channel protein
C;Keywords: duplication

  Query Match             28.6%;  Score 8;  DB 2;  Length 103;
  Best Local Similarity   100.0%;  Pred. No. 0.63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 IFLGSFYL 16
              ||||||||
Db         65 IFLGSFYL 72


RESULT 23
T15794
hypothetical protein C42D8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15794
R;Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid C42D8.
A;Reference number: Z18405
A;Accession: T15794
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-245 <HAL>
A;Cross-references: UNIPROT:Q18582; EMBL:U56966; NID:g1293844; PID:g1293849; PIDN:AAA987
A;Experimental source: strain Bristol N2; clone C42D8
C;Genetics:
A;Gene: CESP:C42D8.1
A;Map position: X
A;Introns: 16/2; 62/3; 90/3; 123/3; 159/3; 208/3

  Query Match             28.6%;  Score 8;  DB 2;  Length 245;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVLVIFLG 12
              ||||||||
Db        125 FVLVIFLG 132


RESULT 24
D69611
ABC transporter required for expression of cytochrome bd (ATP-) cydD - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C;Accession: D69611
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: D69611
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-575 <KUN>
A;Cross-references: UNIPROT:P94367; GB:Z99123; GB:AL009126; NID:g2636240; PIDN:CAB15899.
A;Experimental source: strain 168
C;Genetics:
A;Gene: cydD
C;Superfamily: ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;353-546/Domain: ATP-binding cassette homology <ABC>
F;370-377/Region: nucleotide-binding motif A (P-loop)

  Query Match             28.6%;  Score 8;  DB 2;  Length 575;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVLVIFLG 12
              ||||||||
Db         18 FVLVIFLG 25


RESULT 25
S60051
sodium channel alpha chain, exon c-containing splice form - fruit fly (Drosophila virili
C;Species: Drosophila virilis
C;Date: 24-Aug-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C;Accession: S60051
R;Thackeray, J.R.; Ganetzky, B.
Genetics 141, 203-214, 1995
A;Title: Conserved alternative splicing patterns and splicing signals in the Drosophila
A;Reference number: S60051; MUID:96042905; PMID:8536968
A;Accession: S60051
A;Status: nucleic acid sequence not shown
A;Molecule type: nucleic acid
A;Residues: 1-1034 <THA>
A;Cross-references: UNIPROT:Q24714; EMBL:U26343
C;Genetics:
A;Gene: FlyBase:Dvir/para
A;Cross-references: FlyBase:FBgn0015214
C;Superfamily: sodium channel protein
C;Keywords: alternative splicing; duplication; transmembrane protein
F;306-329/Region: alternatively spliced segment i (exon 4) #status experimental
F;330-350/Region: alternatively spliced exon a #status experimental
F;538-545/Region: alternatively spliced segment b (exon 9) #status experimental
F;874-886/Region: alternatively spliced segment e (exon 12) #status experimental
F;887-896/Region: alternatively spliced segment f (exon 13) #status experimental
F;958-982/Region: alternatively spliced segment h (exon 14) #status experimental

  Query Match             28.6%;  Score 8;  DB 2;  Length 1034;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 IFLGSFYL 16
              ||||||||
Db        188 IFLGSFYL 195
```

Search completed: January 27, 2005, 17:52:42
Job time : 20 secs

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:35:20 ; Search time 92.5 Seconds
(without alignments)
174.167 Million cell updates/sec

Title: US-10-608-584-1
Perfect score: 28
Sequence: 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	100.0	506	2	Q86X25	Q86x25 homo sapien
2	28	100.0	510	2	Q86XY2	Q86xy2 homo sapien
3	28	100.0	1981	2	Q8IUJ6	Q8iuj6 homo sapien
4	28	100.0	2005	1	CIN2_HUMAN	Q99250 homo sapien
5	28	100.0	2005	1	CIN2_RAT	P04775 rattus norv
6	28	100.0	2009	1	CIN1_HUMAN	P35498 homo sapien
7	28	100.0	2009	1	CIN1_RAT	P04774 rattus norv
8	21	75.0	213	2	O42419	O42419 gallus gall
9	21	75.0	225	2	O42420	O42420 gallus gall
10	21	75.0	247	2	Q9IBD6	Q9ibd6 takifugu pa
11	21	75.0	1820	1	CINA_ELEEL	P02719 electrophor
12	21	75.0	1880	2	Q9IBF1	Q9ibf1 takifugu pa
13	21	75.0	1977	2	Q15858	Q15858 homo sapien
14	21	75.0	1984	2	Q28644	Q28644 oryctolagus
15	21	75.0	1984	2	O08562	O08562 rattus norv
16	21	75.0	2049	2	Q25150	Q25150 halocynthia
17	20	71.4	1836	1	CIN4_HUMAN	P35499 homo sapien
18	20	71.4	1840	1	CIN4_RAT	P15390 rattus norv
19	20	71.4	1840	2	O70611	O70611 rattus norv
20	20	71.4	1841	2	Q9ER60	Q9er60 mus musculu
21	16	57.1	530	2	Q90518	Q90518 fugu rubrip
22	16	57.1	711	2	Q803T8	Q803t8 brachydanio
23	16	57.1	1834	2	Q28371	Q28371 equus cabal
24	16	57.1	1951	1	CIN3_RAT	P08104 rattus norv
25	16	57.1	1951	2	Q9C007	Q9c007 homo sapien
26	16	57.1	1956	2	Q9Y5Y9	Q9y5y9 homo sapien
27	16	57.1	2000	1	CIN3_HUMAN	Q9ny46 homo sapien
28	16	57.1	2007	2	Q9YGN7	Q9ygn7 cynops pyrr
29	13	46.4	1956	2	Q62968	Q62968 rattus norv
30	13	46.4	1957	2	Q6QIY3	Q6qiy3 mus musculu
31	13	46.4	1957	2	Q63554	Q63554 rattus norv
32	13	46.4	1957	2	AAS45602	Aas45602 mus muscu
33	13	46.4	1958	2	P70276	P70276 mus musculu
34	13	46.4	1962	2	O46669	O46669 canis famil
35	12	42.9	1444	2	Q9UHM0	Q9uhm0 homo sapien
36	12	42.9	1791	2	Q8NDX3	Q8ndx3 homo sapien
37	12	42.9	1791	2	Q9UHE0	Q9uhe0 homo sapien
38	12	42.9	1791	2	Q9UI33	Q9ui33 homo sapien
39	11	39.3	1136	2	Q804F4	Q804f4 sternopygus
40	11	39.3	1717	2	Q90519	Q90519 fugu rubrip
41	11	39.3	1949	2	Q9DF53	Q9df53 brachydanio
42	11	39.3	1962	2	Q75RX9	Q75rx9 homo sapien
43	11	39.3	1962	2	BAD12085	Bad12085 homo sapi
44	11	39.3	1966	2	Q925G6	Q925g6 rattus norv
45	11	39.3	1976	2	Q63541	Q63541 rattus norv
46	11	39.3	1978	1	CIN8_MOUSE	Q9wtu3 mus musculu
47	11	39.3	1978	2	O88420	O88420 rattus norv
48	11	39.3	1980	1	CIN8_HUMAN	Q9uqd0 homo sapien
49	11	39.3	1988	2	O88421	O88421 rattus norv
50	11	39.3	2013	2	Q865W3	Q865w3 canis famil
51	11	39.3	2015	2	Q86UR3	Q86ur3 homo sapien
52	11	39.3	2015	2	Q8IZC9	Q8izc9 homo sapien
53	11	39.3	2015	2	Q96J69	Q96j69 homo sapien
54	11	39.3	2016	1	CIN5_HUMAN	Q14524 homo sapien
55	11	39.3	2016	2	Q75RY0	Q75ry0 homo sapien
56	11	39.3	2016	2	BAD12084	Bad12084 homo sapi
57	11	39.3	2019	1	CIN5_RAT	P15389 rattus norv
58	11	39.3	2019	2	Q9JJV9	Q9jjv9 mus musculu
59	11	39.3	2022	2	Q8WMP8	Q8wmp8 bos taurus
60	10	35.7	207	2	O42421	O42421 gallus gall
61	10	35.7	211	2	O42418	O42418 gallus gall
62	10	35.7	1784	2	Q25377	Q25377 loligo opal
63	9	32.1	286	2	Q00321	Q00321 lycopersico
64	9	32.1	286	2	Q40039	Q40039 hordeum vul
65	9	32.1	1765	2	O88457	O88457 rattus norv
66	9	32.1	1765	2	Q9JMD4	Q9jmd4 mus musculu
67	9	32.1	1765	2	Q9R053	Q9r053 mus musculu
68	8	28.6	60	2	Q8N0R3	Q8n0r3 plutella xy
69	8	28.6	65	2	Q868A9	Q868a9 drosophila
70	8	28.6	80	2	Q7KQ27	Q7kq27 heliothis v
71	8	28.6	269	2	Q18582	Q18582 caenorhabdi
72	8	28.6	305	2	Q7JPG9	Q7jpg9 drosophila
73	8	28.6	329	2	Q24719	Q24719 drosophila
74	8	28.6	362	2	Q7JN89	Q7jn89 drosophila
75	8	28.6	501	2	Q6DLT8	Q6dlt8 aedes albop
76	8	28.6	509	2	Q6DLT7	Q6dlt7 aedes albop
77	8	28.6	525	2	Q6DLT9	Q6dlt9 aedes albop
78	8	28.6	530	2	Q6DLU0	Q6dlu0 aedes aegyp
79	8	28.6	575	1	CYDD_BACSU	P94367 bacillus su
80	8	28.6	1087	2	Q9XYM6	Q9xym6 leptinotars
81	8	28.6	1538	2	Q7PF76	Q7pf76 anopheles g
82	8	28.6	1618	2	Q8MMC7	Q8mmc7 drosophila
83	8	28.6	1689	2	Q93135	Q93135 blattella g
84	8	28.6	1695	2	Q94584	Q94584 heliothis v
85	8	28.6	2031	2	O01306	O01306 blattella g
86	8	28.6	2031	2	O01307	O01307 blattella g
87	8	28.6	2051	2	Q86DI7	Q86di7 pediculus h
88	8	28.6	2051	2	Q86DI8	Q86di8 pediculus h
89	8	28.6	2051	2	Q86DI9	Q86di9 pediculus h
90	8	28.6	2058	2	Q6DLT4	Q6dlt4 aedes albop
91	8	28.6	2064	2	Q6DLT3	Q6dlt3 aedes aegyp
92	8	28.6	2086	2	Q86M38	Q86m38 pediculus h
93	8	28.6	2104	2	Q25440	Q25440 musca domes
94	8	28.6	2105	2	Q25439	Q25439 musca domes
95	8	28.6	2108	2	Q94615	Q94615 musca domes
96	8	28.6	2131	1	CINA_DROME	P35500 drosophila
97	8	28.6	2215	2	Q86D77	Q86d77 varroa dest
98	8	28.6	2223	2	Q7QIV0	Q7qiv0 anopheles g
99	8	28.6	2304	2	Q9BMQ4	Q9bmq4 blattella g
100	8	28.6	2327	2	Q9W0Y8	Q9w0y8 drosophila

ALIGNMENTS

```
RESULT 1
Q86X25
ID   Q86X25      PRELIMINARY;      PRT;   506 AA.
AC   Q86X25;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to sodium channel, voltage-gated, type II, alpha 2 polypeptide
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC047398; AAH47398.1; -.
DR   HSSP; P08104; 1QG9.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER     506    506
SQ   SEQUENCE   506 AA;  57147 MW;  39C32369D2A96D39 CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 506;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428


RESULT 2
Q86XY2
ID   Q86XY2      PRELIMINARY;      PRT;   510 AA.
AC   Q86XY2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to sodium channel, voltage-gated, type II, alpha 2
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC048417; AAH48417.1; -.
DR   HSSP; P08104; 1QG9.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER     510    510
SQ   SEQUENCE   510 AA;  57660 MW;  CFB153E259C32369 CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 510;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428


RESULT 3
Q8IUJ6
ID   Q8IUJ6      PRELIMINARY;      PRT;  1981 AA.
AC   Q8IUJ6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel alpha 1 subunit.
GN   Name=SCN1A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Normal brain;
RA   Ouchida M., Ohmori I.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AB098335; BAC45228.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008051; Na_channel1.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   InterPro; IPR000100; Ribonuclease_P.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01664; NACHANNEL1.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS00648; RIBONUCLEASE_P; UNKNOWN_1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1981 AA;  226201 MW;  B1D6946D6491B7AD CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 1981;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426


RESULT 4
CIN2_HUMAN
ID   CIN2_HUMAN     STANDARD;      PRT;  2005 AA.
AC   Q99250; Q14472; Q9BZC9; Q9BZD0;
DT   01-JUN-1994 (Rel. 29, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type II alpha subunit (Voltage-gated sodium
```

```
DE   channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha
DE   subunit) (HBSC II).
GN   Name=SCN2A; Synonyms=SCN2A2, NAC2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=92390418; PubMed=1325650;
RA   Ahmed C.M., Ware D.H., Lee S.C., Patten C.D., Ferrer-Montiel A.V.,
RA   Schinder A.F., McPherson J.D., Wagner-Mcpherson C.B., Wasmuth J.J.,
RA   Evans G.A., Montal M.;
RT   "Primary structure, chromosomal localization, and functional
RT   expression of a voltage-gated sodium channel from human brain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:8220-8224(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX   MEDLINE=21142400; PubMed=11245985; DOI=10.1016/S0378-1119(00)00594-1;
RA   Kasai N., Fukushima K., Ueki Y., Prasad S., Nosakowski J.,
RA   Sugata K.-I., Sugata A., Nishizaki K., Meyer N.C., Smith R.J.H.;
RT   "Genomic structures of SCN2A and SCN3A - candidate genes for deafness
RT   at the DFNA16 locus.";
RL   Gene 264:113-122(2001).
RN   [3]
RP   SEQUENCE OF 1-89 FROM N.A.
RA   Lu C.-M., Eichelberger J.S., Beckman M.L., Schade S.D., Brown G.B.;
RT   "Isolation of the 5'-flanking region for human brain sodium channel
RT   subtype II alpha-Subunit (SCN2A).";
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1702-2005 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92275082; PubMed=1317301;
RA   Lu C.-M., Han J., Rado T.A., Brown G.B.;
RT   "Differential expression of two sodium channel subtypes in human
RT   brain.";
RL   FEBS Lett. 303:53-58(1992).
RN   [5]
RP   SEQUENCE OF 1702-1772 FROM N.A.
RX   MEDLINE=91110524; PubMed=1846440;
RA   Han J., Lu C.-M., Brown G.B., Rado T.A.;
RT   "Direct amplification of a single dissected chromosomal segment by
RT   polymerase chain reaction: a human brain sodium channel gene is on
RT   chromosome 2q22-q23.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:335-339(1991).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Adult, 6A;
CC         IsoId=Q99250-1; Sequence=Displayed;
CC       Name=2; Synonyms=Neonatal, 6N;
CC         IsoId=Q99250-2; Sequence=VSP_001032;
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M94055; AAA18895.1; -.
DR   EMBL; AF059683; AAC14574.1; -.
DR   EMBL; AF327246; AAG53413.1; -.
DR   EMBL; AF327226; AAG53413.1; JOINED.
DR   EMBL; AF327227; AAG53413.1; JOINED.
DR   EMBL; AF327228; AAG53413.1; JOINED.
DR   EMBL; AF327229; AAG53413.1; JOINED.
DR   EMBL; AF327230; AAG53413.1; JOINED.
DR   EMBL; AF327231; AAG53413.1; JOINED.
DR   EMBL; AF327232; AAG53413.1; JOINED.
DR   EMBL; AF327233; AAG53413.1; JOINED.
DR   EMBL; AF327234; AAG53413.1; JOINED.
DR   EMBL; AF327235; AAG53413.1; JOINED.
DR   EMBL; AF327236; AAG53413.1; JOINED.
DR   EMBL; AF327237; AAG53413.1; JOINED.
DR   EMBL; AF327238; AAG53413.1; JOINED.
DR   EMBL; AF327239; AAG53413.1; JOINED.
DR   EMBL; AF327240; AAG53413.1; JOINED.
DR   EMBL; AF327241; AAG53413.1; JOINED.
DR   EMBL; AF327242; AAG53413.1; JOINED.
DR   EMBL; AF327243; AAG53413.1; JOINED.
DR   EMBL; AF327244; AAG53413.1; JOINED.
DR   EMBL; AF327245; AAG53413.1; JOINED.
DR   EMBL; AF327246; AAG53412.1; -.
DR   EMBL; AF327226; AAG53412.1; JOINED.
DR   EMBL; AF327227; AAG53412.1; JOINED.
DR   EMBL; AF327228; AAG53412.1; JOINED.
DR   EMBL; AF327229; AAG53412.1; JOINED.
DR   EMBL; AF327230; AAG53412.1; JOINED.
DR   EMBL; AF327231; AAG53412.1; JOINED.
DR   EMBL; AF327232; AAG53412.1; JOINED.
DR   EMBL; AF327233; AAG53412.1; JOINED.
DR   EMBL; AF327234; AAG53412.1; JOINED.
DR   EMBL; AF327235; AAG53412.1; JOINED.
DR   EMBL; AF327236; AAG53412.1; JOINED.
DR   EMBL; AF327237; AAG53412.1; JOINED.
DR   EMBL; AF327238; AAG53412.1; JOINED.
DR   EMBL; AF327239; AAG53412.1; JOINED.
DR   EMBL; AF327240; AAG53412.1; JOINED.
DR   EMBL; AF327241; AAG53412.1; JOINED.
DR   EMBL; AF327242; AAG53412.1; JOINED.
DR   EMBL; AF327243; AAG53412.1; JOINED.
DR   EMBL; AF327244; AAG53412.1; JOINED.
DR   EMBL; AF327245; AAG53412.1; JOINED.
DR   EMBL; X65361; CAA46438.1; ALT_SEQ.
DR   EMBL; M91804; -; NOT_ANNOTATED_CDS.
DR   EMBL; M55662; AAB65854.2; -.
DR   HSSP; P04775; 1BYY.
DR   Genew; HGNC:10588; SCN2A2.
DR   MIM; 601219; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; TAS.
DR   GO; GO:0006814; P:sodium ion transport; TAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   REPEAT      111    456       I.
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```
FT   REPEAT       741   1013       II.
FT   REPEAT      1190   1504       III.
FT   REPEAT      1513   1811       IV.
FT   TRANSMEM     125    148       S1 of repeat I.
FT   TRANSMEM     157    176       S2 of repeat I.
FT   TRANSMEM     190    208       S3 of repeat I.
FT   TRANSMEM     215    234       S4 of repeat I.
FT   TRANSMEM     251    274       S5 of repeat I.
FT   TRANSMEM     402    427       S6 of repeat I.
FT   TRANSMEM     754    778       S1 of repeat II.
FT   TRANSMEM     790    813       S2 of repeat II.
FT   TRANSMEM     822    841       S3 of repeat II.
FT   TRANSMEM     848    867       S4 of repeat II.
FT   TRANSMEM     884    904       S5 of repeat II.
FT   TRANSMEM     958    983       S6 of repeat II.
FT   TRANSMEM    1204   1227       S1 of repeat III.
FT   TRANSMEM    1241   1266       S2 of repeat III.
FT   TRANSMEM    1273   1294       S3 of repeat III.
FT   TRANSMEM    1299   1320       S4 of repeat III.
FT   TRANSMEM    1340   1367       S5 of repeat III.
FT   TRANSMEM    1447   1473       S6 of repeat III.
FT   TRANSMEM    1527   1550       S1 of repeat IV.
FT   TRANSMEM    1562   1585       S2 of repeat IV.
FT   TRANSMEM    1592   1615       S3 of repeat IV.
FT   TRANSMEM    1626   1647       S4 of repeat IV.
FT   TRANSMEM    1663   1685       S5 of repeat IV.
FT   TRANSMEM    1752   1776       S6 of repeat IV.
FT   DOMAIN      1905   1934       IQ.
FT   CARBOHYD     212    212       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     285    285       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     291    291       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     297    297       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     303    303       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     340    340       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     604    604       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     624    624       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     883    883       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1055   1055       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1072   1072       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1136   1136       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1368   1368       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1382   1382       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1393   1393       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1778   1778       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC     209    209       D -> N (in isoform 2).
FT                                  /FTId=VSP_001032.
FT   CONFLICT     524    524       R -> L (in Ref. 1).
```

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  Query Match           100.0%;  Score 28;  DB 1;  Length 2005;
  Best Local Similarity  100.0%;  Pred. No. 7.2e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428
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RESULT 5
CIN2_RAT
ID   CIN2_RAT       STANDARD;      PRT;  2005 AA.
AC   P04775;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Sodium channel protein type II alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha
DE   subunit).
GN   Name=Scn2a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86146901; PubMed=3754035;
RA   Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M.,
RA   Takahashi H., Numa S.;
RT   "Existence of distinct sodium channel messenger RNAs in rat brain.";
RL   Nature 320:188-192(1986).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X03639; CAA27287.1; -.
DR   PDB; 1BYY; NMR; A=1474-1526.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   3D-structure; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   REPEAT       111    456       I.
FT   REPEAT       741   1013       II.
FT   REPEAT      1190   1504       III.
FT   REPEAT      1513   1811       IV.
FT   TRANSMEM     125    148       S1 of repeat I.
FT   TRANSMEM     157    176       S2 of repeat I.
FT   TRANSMEM     190    208       S3 of repeat I.
FT   TRANSMEM     215    234       S4 of repeat I.
FT   TRANSMEM     251    274       S5 of repeat I.
FT   TRANSMEM     402    427       S6 of repeat I.
FT   TRANSMEM     754    778       S1 of repeat II.
FT   TRANSMEM     790    813       S2 of repeat II.
FT   TRANSMEM     822    841       S3 of repeat II.
FT   TRANSMEM     848    867       S4 of repeat II.
FT   TRANSMEM     884    904       S5 of repeat II.
FT   TRANSMEM     958    983       S6 of repeat II.
FT   TRANSMEM    1204   1227       S1 of repeat III.
FT   TRANSMEM    1241   1266       S2 of repeat III.
FT   TRANSMEM    1273   1294       S3 of repeat III.
FT   TRANSMEM    1299   1320       S4 of repeat III.
FT   TRANSMEM    1340   1367       S5 of repeat III.
FT   TRANSMEM    1447   1473       S6 of repeat III.
FT   TRANSMEM    1527   1550       S1 of repeat IV.
FT   TRANSMEM    1562   1585       S2 of repeat IV.
FT   TRANSMEM    1592   1615       S3 of repeat IV.
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FT   TRANSMEM    1626   1647       S4 of repeat IV.
FT   TRANSMEM    1663   1685       S5 of repeat IV.
FT   TRANSMEM    1752   1776       S6 of repeat IV.
FT   DOMAIN      1905   1934       IQ.
FT   CARBOHYD     212    212       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     285    285       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     291    291       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     297    297       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     303    303       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     340    340       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     604    604       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     624    624       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     883    883       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1055   1055       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1072   1072       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1136   1136       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1368   1368       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1382   1382       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1393   1393       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   2005 AA;  227872 MW;  861BE583D79F8324 CRC64;

  Query Match             100.0%;  Score 28;  DB 1;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428


RESULT 6
CIN1_HUMAN
ID   CIN1_HUMAN     STANDARD;      PRT;  2009 AA.
AC   P35498; Q16172; Q96LA3; Q9C008;
DT   01-JUN-1994 (Rel. 29, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type I alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.1) (Sodium channel protein, brain I alpha
DE   subunit).
GN   Name=SCN1A; Synonyms=SCN1, NAC1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS GEFS+2 MET-875 AND
RP   HIS-1648.
RX   MEDLINE=20206553; PubMed=10742094;
RA   Escayg A., MacDonald B.T., Meisler M.H., Baulac S., Huberfeld G.,
RA   An-Gourfinkel I., Brice A., LeGuern E., Moulard B., Chaigne D.,
RA   Buresi C., Malafosse A.;
RT   "Mutations of SCN1A, encoding a neuronal sodium channel, in two
RT   families with GEFS+2.";
RL   Nat. Genet. 24:343-345(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RA   Jeong S.-Y., Goto J., Kanazawa I.;
RT   "Cloning of cDNA for human voltage-gated sodium channel alpha subunit,
RT   SCN1A.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Brain;
RA   Sugawara T., Mazaki E.M., Yamakawa K.;
RT   "Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1)
RT   mRNA.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT THR-1067.
RA   Ouchida M., Ohmori I.;
RT   "Isoforms of human sodium channel SCN1A gene.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 1335-1428 FROM N.A.
RX   MEDLINE=94340991; PubMed=8062593;
RA   Malo M.S., Blanchard B.J., Andresen J.M., Srivastava K., Chen X.N.,
RA   Li X., Jabs E.W., Korenberg J.R., Ingram V.M.;
RT   "Localization of a putative human brain sodium channel gene (SCN1A) to
RT   chromosome band 2q24.";
RL   Cytogenet. Cell Genet. 67:178-186(1994).
RN   [6]
RP   SEQUENCE OF 1518-1940 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92275082; PubMed=1317301;
RA   Lu C.-M., Han J., Rado T.A., Brown G.B.;
RT   "Differential expression of two sodium channel subtypes in human
RT   brain.";
RL   FEBS Lett. 303:53-58(1992).
RN   [7]
RP   VARIANTS GEFS+2 VAL-188; LEU-1353 AND MET-1656.
RX   MEDLINE=21152274; PubMed=11254444;
RA   Wallace R.H., Scheffer I.E., Barnett S., Richards M., Dibbens L.,
RA   Desai R.R., Lerman-Sagie T., Lev D., Mazarib A., Brand N.,
RA   Ben-Zeev B., Goikhman I., Singh R., Kremmidiotis G., Gardner A.,
RA   Sutherland G.R., George A.L. Jr., Mulley J.C., Berkovic S.F.;
RT   "Neuronal sodium-channel alpha1-subunit mutations in generalized
RT   epilepsy with febrile seizures plus.";
RL   Am. J. Hum. Genet. 68:859-865(2001).
RN   [8]
RP   VARIANT GEFS+2 ARG-1204.
RX   MEDLINE=21152275; PubMed=11254445;
RA   Escayg A., Heils A., MacDonald B.T., Haug K., Sander T., Meisler M.H.;
RT   "A novel SCN1A mutation associated with generalized epilepsy with
RT   febrile seizures plus -- and prevalence of variants in patients with
RT   epilepsy.";
RL   Am. J. Hum. Genet. 68:866-873(2001).
RN   [9]
RP   VARIANT SMEI PHE-986.
RX   MEDLINE=21257503; PubMed=11359211;
RA   Claes L., Del-Favero J., Ceulemans B., Lagae L., Van Broeckhoven C.,
RA   De Jonghe P.;
RT   "De novo mutations in the sodium-channel gene SCN1A cause severe
RT   myoclonic epilepsy of infancy.";
RL   Am. J. Hum. Genet. 68:1327-1332(2001).
RN   [10]
RP   VARIANT GEFS+2 THR-1270.
RX   MEDLINE=21630138; PubMed=11756608;
RA   Abou-Khalil B., Ge Q., Desai R., Ryther R., Bazyk A., Bailey R.,
RA   Haines J.L., Sutcliffe J.S., George A.L. Jr.;
RT   "Partial and generalized epilepsy with febrile seizures plus and a
RT   novel SCN1A mutation.";
RL   Neurology 57:2265-2272(2001).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=P35498-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P35498-2; Sequence=VSP_001031;
CC         Note=No experimental confirmation available;
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- DISEASE: Defects in SCN1A are the cause of generalized epilepsy
CC       with febrile seizures plus type 2 (GEFS+2) [MIM:604233]. This
```

```
CC       autosomal dominant disorder is characterized by febrile seizures
CC       in children and afebrile seizures in adults. Penetrance is
CC       incomplete and a large intrafamilial variability of the phenotype
CC       is observed.
CC   -!- DISEASE: Defects in SCN1A are a cause of severe myoclonic epilepsy
CC       in infancy (SMEI) [MIM:607208], a severe form of generalized
CC       epilepsy with febrile seizures. SMEI is a rare disorder
CC       characterized by normal development before onset, seizures
CC       beginning in the first year of life in the form of generalized or
CC       unilateral febrile clonic seizures, secondary appearance of
CC       myoclonic seizures, and occasionally partial seizures. It is
CC       associated with ataxia, slowed psychomotor development, and mental
CC       decline.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF225985; AAK00217.1; -.
DR   EMBL; AY043484; AAK95360.1; -.
DR   EMBL; AB093548; BAC21101.1; -.
DR   EMBL; AB093549; BAC21102.1; -.
DR   EMBL; S71446; AAB31605.1; -.
DR   EMBL; X65362; CAA46439.1; -.
DR   EMBL; M91803; -; NOT_ANNOTATED_CDS.
DR   PIR; I52964; I52964.
DR   PIR; S29184; S29184.
DR   HSSP; P04775; 1BYY.
DR   Genew; HGNC:10585; SCN1A.
DR   MIM; 182389; -.
DR   MIM; 604233; -.
DR   MIM; 607208; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; NAS.
DR   GO; GO:0006814; P:sodium ion transport; NAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008051; Na_channel1.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01664; NACHANNEL1.
DR   PROSITE; PS50096; IQ; FALSE_NEG.
KW   Alternative splicing; Disease mutation; Epilepsy; Glycoprotein;
KW   Ion transport; Ionic channel; Multigene family; Polymorphism; Repeat;
KW   Sodium channel; Transmembrane; Voltage-gated channel.
FT   REPEAT      110    454       I.
FT   REPEAT      750   1022       II.
FT   REPEAT     1200   1514       III.
FT   REPEAT     1523   1821       IV.
FT   TRANSMEM    124    147       S1 of repeat I (By similarity).
FT   TRANSMEM    156    175       S2 of repeat I (By similarity).
FT   TRANSMEM    189    207       S3 of repeat I (By similarity).
FT   TRANSMEM    214    233       S4 of repeat I (By similarity).
FT   TRANSMEM    250    273       S5 of repeat I (By similarity).
FT   TRANSMEM    400    425       S6 of repeat I (By similarity).
FT   TRANSMEM    763    787       S1 of repeat II (By similarity).
FT   TRANSMEM    799    822       S2 of repeat II (By similarity).
FT   TRANSMEM    831    850       S3 of repeat II (By similarity).
FT   TRANSMEM    857    876       S4 of repeat II (By similarity).
FT   TRANSMEM    893    913       S5 of repeat II (By similarity).
FT   TRANSMEM    967    992       S6 of repeat II (By similarity).
FT   TRANSMEM   1214   1237       S1 of repeat III (By similarity).
FT   TRANSMEM   1251   1276       S2 of repeat III (By similarity).
FT   TRANSMEM   1283   1304       S3 of repeat III (By similarity).
FT   TRANSMEM   1309   1330       S4 of repeat III (By similarity).
FT   TRANSMEM   1350   1377       S5 of repeat III (By similarity).
FT   TRANSMEM   1457   1483       S6 of repeat III (By similarity).
FT   TRANSMEM   1537   1560       S1 of repeat IV (By similarity).
FT   TRANSMEM   1572   1595       S2 of repeat IV (By similarity).
FT   TRANSMEM   1602   1625       S3 of repeat IV (By similarity).
FT   TRANSMEM   1636   1657       S4 of repeat IV (By similarity).
FT   TRANSMEM   1673   1695       S5 of repeat IV (By similarity).
FT   TRANSMEM   1762   1786       S6 of repeat IV (By similarity).
FT   CARBOHYD    211    211       N-linked (GlcNAc. . .) (Potential).
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  Query Match             100.0%;  Score 28;  DB 1;  Length 2009;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426
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RESULT 7
CIN1_RAT
ID   CIN1_RAT       STANDARD;      PRT;  2009 AA.
AC   P04774;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type I alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.1) (Sodium channel protein, brain I alpha
DE   subunit).
GN   Name=Scn1a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86146901; PubMed=3754035;
RA   Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M.,
RA   Takahashi H., Numa S.;
RT   "Existence of distinct sodium channel messenger RNAs in rat brain.";
RL   Nature 320:188-192(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87311395; PubMed=2442385;
RA   Noda M., Numa S.;
RT   "Structure and function of sodium channel.";
RL   J. Recept. Res. 7:467-497(1987).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; X03638; CAA27286.1; -.
DR   EMBL; M22253; AAA79965.1; -.
DR   PIR; A25019; A25019.
DR   HSSP; P04775; 1BYY.
DR   RGD; 69364; Scn1a.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008051; Na_channel1.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01664; NACHANNEL1.
DR   PROSITE; PS50096; IQ; FALSE_NEG.
KW   Glycoprotein; Ion transport; Ionic channel; Multigene family; Repeat;
KW   Sodium channel; Transmembrane; Voltage-gated channel.
FT   REPEAT      110    454       I.
FT   REPEAT      750   1022       II.
FT   REPEAT     1200   1514       III.
FT   REPEAT     1523   1821       IV.
FT   TRANSMEM    124    147       S1 of repeat I.
FT   TRANSMEM    156    175       S2 of repeat I.
FT   TRANSMEM    189    207       S3 of repeat I.
FT   TRANSMEM    214    233       S4 of repeat I.
FT   TRANSMEM    250    273       S5 of repeat I.
FT   TRANSMEM    400    425       S6 of repeat I.
FT   TRANSMEM    763    787       S1 of repeat II.
FT   TRANSMEM    799    822       S2 of repeat II.
FT   TRANSMEM    831    850       S3 of repeat II.
FT   TRANSMEM    857    876       S4 of repeat II.
FT   TRANSMEM    893    913       S5 of repeat II.
FT   TRANSMEM    967    992       S6 of repeat II.
FT   TRANSMEM   1214   1237       S1 of repeat III.
FT   TRANSMEM   1251   1276       S2 of repeat III.
FT   TRANSMEM   1283   1304       S3 of repeat III.
FT   TRANSMEM   1309   1330       S4 of repeat III.
FT   TRANSMEM   1350   1377       S5 of repeat III.
FT   TRANSMEM   1457   1483       S6 of repeat III.
FT   TRANSMEM   1537   1560       S1 of repeat IV.
FT   TRANSMEM   1572   1595       S2 of repeat IV.
FT   TRANSMEM   1602   1625       S3 of repeat IV.
FT   TRANSMEM   1636   1657       S4 of repeat IV.
FT   TRANSMEM   1673   1695       S5 of repeat IV.
FT   TRANSMEM   1762   1786       S6 of repeat IV.
FT   CARBOHYD    211    211       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    284    284       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    295    295       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    301    301       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    306    306       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    338    338       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    601    601       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    621    621       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    681    681       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    892    892       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1060   1060       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1064   1064       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1080   1080       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1146   1146       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1378   1378       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1392   1392       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1403   1403       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   2009 AA;  228769 MW;  6808466F6368373B CRC64;

  Query Match             100.0%;  Score 28;  DB 1;  Length 2009;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||||||||||
Db        399 YMIFFVLVIFLGSFYLINLILAVVAMAY 426


RESULT 8
O42419
ID   O42419      PRELIMINARY;      PRT;   213 AA.
AC   O42419;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Voltage-gated sodium channel I (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dorsal root ganglion;
RX   MEDLINE=98024190; PubMed=9356508;
RA   Friedel R.H., Schnuerch H., Stubbusch J., Barde Y.A.;
RT   "Identification of genes differentially expressed by nerve growth
RT   factor- and neurotrophin-3-dependent sensory neurons.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:12670-12675(1997).
DR   EMBL; AJ001489; CAA04784.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1      1
FT   NON_TER     213    213
SQ   SEQUENCE   213 AA;  24397 MW;  DAF3B6AE4E8E47ED CRC64;

  Query Match             75.0%;  Score 21;  DB 2;  Length 213;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLIL 21
              |||||||||||||||||||||
Db        193 YMIFFVLVIFLGSFYLINLIL 213


RESULT 9
O42420
ID   O42420      PRELIMINARY;      PRT;   225 AA.
AC   O42420;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Voltage-gated sodium channel II (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dorsal root ganglion;
RX   MEDLINE=98024190; PubMed=9356508;
RA   Friedel R.H., Schnuerch H., Stubbusch J., Barde Y.A.;
RT   "Identification of genes differentially expressed by nerve growth
RT   factor- and neurotrophin-3-dependent sensory neurons.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:12670-12675(1997).
DR   EMBL; AJ001490; CAA04785.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
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DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1      1
FT   NON_TER     225    225
SQ   SEQUENCE   225 AA;  25531 MW;  85B122E582F3023E CRC64;

  Query Match             75.0%;  Score 21;  DB 2;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYLINLIL 21
              |||||||||||||||||||||
Db        205 YMIFFVLVIFLGSFYLINLIL 225


RESULT 10
Q9IBD6
ID   Q9IBD6       PRELIMINARY;      PRT;   247 AA.
AC   Q9IBD6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Skeletal muscle voltage-gated sodium channel (FMNa2) (Fragment).
OS   Takifugu pardalis (Panther puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=98921;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=20090650; PubMed=10623632;
RA   Yotsu-Yamashita M., Nishimori K., Nitanai Y., Isemura M., Sugimoto A.,
RA   Yasumoto T.;
RT   "Binding properties of 3H-PbTx-3 and 3H-saxitoxin to brain membranes
RT   and to skeletal muscle membranes of puffer fish Fugu pardalis, and the
RT   primary structure of a voltage-gated Na+ channel alpha-subunit (fMNa1)
RT   from skeletal muscle of F. pardalis.";
RL   Biochem. Biophys. Res. Commun. 267:403-412(2000).
DR   EMBL; AB032022; BAA90308.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1      1
FT   NON_TER     247    247
SQ   SEQUENCE   247 AA;  27998 MW;  0B8C1CECEF05E1F5 CRC64;

  Query Match             75.0%;  Score 21;  DB 2;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        223 VIFLGSFYLINLILAVVAMAY 243


RESULT 11
CINA_ELEEL
ID   CINA_ELEEL     STANDARD;      PRT;  1820 AA.
AC   P02719;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   29-MAR-2004 (Rel. 43, Last annotation update)
DE   Sodium channel protein (Na(+) channel).
OS   Electrophorus electricus (Electric eel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC   Electrophoridae; Electrophorus.
OX   NCBI_TaxID=8005;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85061498; PubMed=6209577;
RA   Noda M., Shimizu S., Tanabe T., Takai T., Kayano T., Ikeda T.,
RA   Takahashi H., Nakayama H., Kanaoka Y., Minamino N., Kangawa K.,
RA   Matsuo H., Raftery M.A., Hirose T., Inayama S., Hayashida H.,
RA   Miyata T., Numa S.;
RT   "Primary structure of Electrophorus electricus sodium channel deduced
RT   from cDNA sequence.";
RL   Nature 312:121-127(1984).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87311395; PubMed=2442385;
RA   Noda M., Numa S.;
RT   "Structure and function of sodium channel.";
RL   J. Recept. Res. 7:467-497(1987).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- MISCELLANEOUS: Available data suggest that activation and
CC       inactivation gates are located near the cytoplasmic surface of the
CC       membrane. It is hypothesized that residues 802-806, 847-857, 894-
CC       910, and 942-955 might, in conjunction with the positively charged
CC       residues of S4, act as a voltage sensor involved with the
CC       activation gate.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X01119; CAA25587.1; -.
DR   EMBL; M22252; AAA79960.1; -.
DR   PIR; A03178; CHEE.
DR   HSSP; P04775; 1BYY.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; FALSE_NEG.
KW   Glycoprotein; Ion transport; Ionic channel; Repeat; Sodium channel;
KW   Transmembrane; Voltage-gated channel.
FT   REPEAT      111    419       I.
FT   REPEAT      555    807       II.
FT   REPEAT      989   1281       III.
FT   REPEAT     1311   1587       IV.
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FT   TRANSMEM    118    138       S1 of repeat I.
FT   TRANSMEM    150    171       S2 of repeat I.
FT   TRANSMEM    177    197       S3 of repeat I.
FT   TRANSMEM    204    224       S4 of repeat I.
FT   TRANSMEM    244    264       S5 of repeat I.
FT   DOMAIN      285    342       Non-homologous region of repeat I.
FT   TRANSMEM    379    402       S6 of repeat I.
FT   TRANSMEM    558    578       S1 of repeat II.
FT   TRANSMEM    600    620       S2 of repeat II.
FT   TRANSMEM    626    643       S3 of repeat II.
FT   TRANSMEM    651    671       S4 of repeat II.
FT   TRANSMEM    691    711       S5 of repeat II.
FT   TRANSMEM    767    790       S6 of repeat II.
FT   TRANSMEM   1005   1025       S1 of repeat III.
FT   TRANSMEM   1038   1058       S2 of repeat III.
FT   TRANSMEM   1066   1086       S3 of repeat III.
FT   TRANSMEM   1092   1112       S4 of repeat III.
FT   TRANSMEM   1132   1152       S5 of repeat III.
FT   DOMAIN     1172   1194       Non-homologous region of repeat III.
FT   TRANSMEM   1244   1264       S6 of repeat III.
FT   TRANSMEM   1321   1341       S1 of repeat IV.
FT   TRANSMEM   1353   1376       S2 of repeat IV.
FT   TRANSMEM   1381   1398       S3 of repeat IV.
FT   TRANSMEM   1417   1437       S4 of repeat IV.
FT   TRANSMEM   1454   1474       S5 of repeat IV.
FT   DOMAIN     1490   1505       Non-homologous region of repeat IV.
FT   TRANSMEM   1544   1567       S6 of repeat IV.
FT   CARBOHYD    278    278       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    288    288       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    317    317       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    591    591       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    690    690       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    797    797       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1160   1160       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1174   1174       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   1820 AA;  208331 MW;  1B271F626E057864 CRC64;

  Query Match             75.0%;  Score 21;  DB 1;  Length 1820;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        385 VIFLGSFYLINLILAVVAMAY 405


RESULT 12
Q9IBF1
ID   Q9IBF1      PRELIMINARY;      PRT;  1880 AA.
AC   Q9IBF1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel.
OS   Takifugu pardalis (Panther puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=98921;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=20090650; PubMed=10623632;
RA   Yotsu-Yamashita M., Nishimori K., Nitanai Y., Isemura M., Sugimoto A.,
RA   Yasumoto T.;
RT   "Binding properties of 3H-PbTx-3 and 3H-saxitoxin to brain membranes
RT   and to skeletal muscle membranes of puffer fish Fugu pardalis, and the
RT   primary structure of a voltage-gated Na+ channel alpha-subunit (fMNa1)
RT   from skeletal muscle of F. pardalis.";
RL   Biochem. Biophys. Res. Commun. 267:403-412(2000).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AB030482; BAA90398.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1880 AA;  212084 MW;  406483C6C3D43E02 CRC64;

  Query Match             75.0%;  Score 21;  DB 2;  Length 1880;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        405 VIFLGSFYLINLILAVVAMAY 425


RESULT 13
Q15858
ID   Q15858      PRELIMINARY;      PRT;  1977 AA.
AC   Q15858;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel alpha subunit.
GN   Name=hNE-Na;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thyroid;
RX   MEDLINE=95237189; PubMed=7720699;
RA   Klugbauer N., Lacinova L., Flockerzi V., Hofmann F.;
RT   "Structure and functional expression of a new member of the
RT   tetrodotoxin-sensitive voltage-activated sodium channel family from
RT   human neuroendocrine cells.";
RL   EMBO J. 14:1084-1090(1995).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; X82835; CAA58042.1; -.
DR   PIR; S54771; S54771.
DR   HSSP; P04775; 1BYY.
DR   Genew; HGNC:10597; SCN9A.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; TAS.
DR   GO; GO:0006814; P:sodium ion transport; TAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
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DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1977 AA;  225195 MW;  17D67CBC32BC15FB CRC64;

  Query Match             75.0%;  Score 21;  DB 2;  Length 1977;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-11;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        385 VIFLGSFYLINLILAVVAMAY 405


RESULT 14
Q28644
ID   Q28644      PRELIMINARY;      PRT;  1984 AA.
AC   Q28644;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel alpha-subunit.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=New Zealand White; TISSUE=Sciatic nerve;
RX   MEDLINE=96074641; PubMed=7479931;
RA   Belcher S.M., Zerillo C.A., Levenson R., Ritchie J.M., Howe J.R.;
RT   "Cloning of a sodium channel alpha subunit from rabbit Schwann
RT   cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:11034-11038(1995).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; U35238; AAA89159.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1984 AA;  225748 MW;  98F76860C9866AA0 CRC64;

  Query Match             75.0%;  Score 21;  DB 2;  Length 1984;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-11;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        383 VIFLGSFYLINLILAVVAMAY 403


RESULT 15
O08562
ID   O08562      PRELIMINARY;      PRT;  1984 AA.
AC   O08562;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   PN1 (Voltage-gated sodium channel) (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97188502; PubMed=9037087;
RA   Toledo-Aral J.J., Moss B.L., He Z.J., Koszowski A.G., Whisenand T.,
RA   Levinson S.R., Wolf J.J., Silos-Santiago I., Halegoua S., Mandel G.;
RT   "Identification of PN1, a predominant voltage-dependent sodium channel
RT   expressed principally in peripheral neurons.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:1527-1532(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97007982; PubMed=8854872;
RA   Kozak C.A., Sangameswaran L.;
RT   "Genetic mapping of the peripheral sodium channel genes, Scn9a and
RT   Scn10a, in the mouse.";
RL   Mamm. Genome 7:787-788(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Sangameswaran L., Fish L.M., Koch B.D., Rabert D.K., Delgado S.G.,
RA   Ilnicka M., Jakeman L.B., Novakovic S., Wong K., Sze P., Tzoumaka E.,
RA   Stewart G.R., Herman R.C., Chan H., Eglen R.M., Hunter J.C.;
RT   "A novel tetrodotoxin-sensitive, voltage-gated sodium channel
RT   expressed in rat and human dorsal root ganglia.";
RL   J. Biol. Chem. 0:0-0(1997).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; U79568; AAB50403.1; -.
DR   EMBL; AF000368; AAB80701.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
FT   NON_TER    1984   1984
SQ   SEQUENCE   1984 AA;  226037 MW;  386C38B9B5097091 CRC64;

  Query Match             75.0%;  Score 21;  DB 2;  Length 1984;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-11;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        385 VIFLGSFYLINLILAVVAMAY 405


RESULT 16
Q25150
ID   Q25150      PRELIMINARY;      PRT;  2049 AA.
AC   Q25150;
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DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel.
GN   Name=TuNaI;
OS   Halocynthia roretzi (Sea squirt).
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC   Stolidobranchia; Pyuridae; Halocynthia.
OX   NCBI_TaxID=7729;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95033215; PubMed=7946338;
RA   Okamura Y., Ono F., Okagaki R., Chong J., Mandel G.;
RT   "Neural expression of a sodium channel gene requires cell-specific
RT   interactions.";
RL   Neuron 13:937-948(1994).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; D17311; BAA04133.1; -.
DR   PIR; T43161; T43161.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   2049 AA;  233443 MW;  F7DE3578105B73FB CRC64;

  Query Match             75.0%;  Score 21;  DB 2;  Length 2049;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-11;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        449 VIFLGSFYLINLILAVVAMAY 469


RESULT 17
CIN4_HUMAN
ID   CIN4_HUMAN     STANDARD;      PRT;  1836 AA.
AC   P35499; Q15478; Q16447; Q7Z6B1;
DT   01-JUN-1994 (Rel. 29, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type IV alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.4) (Sodium channel protein, skeletal muscle
DE   alpha-subunit).
GN   Name=SCN4A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANT ASP-559.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=92246457; PubMed=1315496;
RA   George A.L. Jr., Komisarof J., Kallen R.G., Barchi R.L.;
RT   "Primary structure of the adult human skeletal muscle voltage-
RT   dependent sodium channel.";
RL   Ann. Neurol. 31:131-137(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92134303; PubMed=1310396;
RA   Wang J., Rojas C.V., Zhou J., Schwartz L.S., Nicholas H.,
RA   Hoffmann E.P.;
RT   "Sequence and genomic structure of the human adult skeletal muscle
RT   sodium channel alpha subunit gene on 17q.";
RL   Biochem. Biophys. Res. Commun. 182:794-801(1992).
RN   [3]
RP   SEQUENCE FROM N.A., VARIANT MYASTHENIC SYNDROME GLU-1442, AND VARIANTS
RP   LEU-246; ASP-559 AND ASN-1376.
RX   MEDLINE=22684480; PubMed=12766226; DOI=10.1073/pnas.1230273100;
RA   Tsujino A., Maertens C., Ohno K., Shen X.-M., Fukuda T., Harper C.M.,
RA   Cannon S.C., Engel A.G.;
RT   "Myasthenic syndrome caused by mutation of the SCN4A sodium channel.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:7377-7382(2003).
RN   [4]
RP   SEQUENCE FROM N.A., AND VARIANT ASN-1376.
RX   MEDLINE=93338444; PubMed=1339144;
RA   McClatchey A.I., Lin C.S., Wang J., Hoffman E.P., Rojas C.V.,
RA   Gusella J.F.;
RT   "The genomic structure of the human skeletal muscle sodium channel
RT   gene.";
RL   Hum. Mol. Genet. 1:521-521(1992).
RN   [5]
RP   SEQUENCE OF 1305-1339 FROM N.A., AND VARIANTS PMC VAL-1306 AND
RP   MET-1313.
RX   MEDLINE=92154689; PubMed=1310898;
RA   McClatchey A.I., van den Bergh P., Pericak-Vance M.A., Raskind W.,
RA   Verellen C., McKenna-Yasek D., Rao K., Haines J.L., Bird T.,
RA   Brown R.H. Jr., Gusella J.F.;
RT   "Temperature-sensitive mutations in the III-IV cytoplasmic loop region
RT   of the skeletal muscle sodium channel gene in paramyotonia
RT   congenita.";
RL   Cell 68:769-774(1992).
RN   [6]
RP   VARIANT HYPP MET-704.
RX   MEDLINE=92069747; PubMed=1659948;
RA   Ptacek L.J., George A.L. Jr., Griggs R.C., Tawil R., Kallen R.G.,
RA   Barchi R.L., Robertson M., Leppert M.F.;
RT   "Identification of a mutation in the gene causing hyperkalemic
RT   periodic paralysis.";
RL   Cell 67:1021-1027(1991).
RN   [7]
RP   VARIANT HYPP VAL-1592.
RX   MEDLINE=92065978; PubMed=1659668;
RA   Rojas C.V., Wang J., Schwartz L.S., Hoffman E.P., Powell B.R.,
RA   Brown R.H. Jr.;
RT   "A Met-to-Val mutation in the skeletal muscle Na+ channel alpha-
RT   subunit in hyperkalaemic periodic paralysis.";
RL   Nature 354:387-389(1991).
RN   [8]
RP   VARIANTS PMC PHE-804 AND THR-1156.
RX   MEDLINE=93265141; PubMed=1338909;
RA   McClatchey A.I., McKenna-Yasek D., Cros D., Worthen H.G., Kuncl R.W.,
RA   Desilva S.M., Cornblath D.R., Gusella J.F., Brown R.H. Jr.;
RT   "Novel mutations in families with unusual and variable disorders of
RT   the skeletal muscle sodium channel.";
RL   Nat. Genet. 2:148-152(1992).
RN   [9]
RP   VARIANTS PMC CYS-1448 AND HIS-1448.
RX   MEDLINE=92265302; PubMed=1316765;
RA   Ptacek L.J., George A.L. Jr., Barchi R.L., Griggs R.C., Riggs J.E.,
RA   Robertson M., Leppert M.F.;
RT   "Mutations in an S4 segment of the adult skeletal muscle sodium
RT   channel cause paramyotonia congenita.";
RL   Neuron 8:891-897(1992).
RN   [10]
RP   VARIANT PMC ARG-1433.
RX   MEDLINE=93270429; PubMed=8388676;
RA   Ptacek L.J., Gouw L., Kwiecinski H., McManis P., Mendell J.R.,
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RA   Barohn R.J., George A.L. Jr., Barchi R.L., Robertson M., Leppert M.F.;
RT   "Sodium channel mutations in paramyotonia congenita and hyperkalemic
RT   periodic paralysis.";
RL   Ann. Neurol. 33:300-307(1993).
RN   [11]
RP   VARIANTS PMC ALA-1306; GLU-1306 AND VAL-1306.
RX   MEDLINE=94141728; PubMed=8308722;
RA   Lerche H., Heine R., Pika U., George A.L. Jr., Mitrovic N.,
RA   Browatzki M., Weiss T., Rivet-Bastide M., Franke C., Lomonaco M.,
RA   Ricker K., Lehmann-Horn F.;
RT   "Human sodium channel myotonia: slowed channel inactivation due to
RT   substitutions for a glycine within the III-IV linker.";
RL   J. Physiol. (Lond.) 470:13-22(1993).
RN   [12]
RP   VARIANT PMC MET-1589.
RX   MEDLINE=94061027; PubMed=8242056;
RA   Heine R., Pika U., Lehmann-Horn F.;
RT   "A novel SCN4A mutation causing myotonia aggravated by cold and
RT   potassium.";
RL   Hum. Mol. Genet. 2:1349-1353(1993).
RN   [13]
RP   VARIANT POTASSIUM-AGGRAVATED MYOTONIA VAL-1160.
RX   PubMed=8058156;
RA   Ptacek L.J., Tawil R., Griggs R.C., Meola G., McManis P., Barohn R.J.,
RA   Mendell J.R., Harris C., Spitzer R., Santiago F., Leppert M.F.;
RT   "Sodium channel mutations in acetazolamide-responsive myotonia
RT   congenita, paramyotonia congenita, and hyperkalemic periodic
RT   paralysis.";
RL   Neurology 44:1500-1503(1994).
RN   [14]
RP   VARIANT PARAMYOTONIA WITHOUT COLD PARALYSIS ILE-1293.
RX   MEDLINE=96154961; PubMed=8580427;
RA   Koch M.C., Baumbach K., George A.L., Ricker K.;
RT   "Paramyotonia congenita without paralysis on exposure to cold: a novel
RT   mutation in the SCN4A gene (Val1293Ile).";
RL   NeuroReport 6:2001-2004(1995).
RN   [15]
RP   VARIANT POTASSIUM-AGGRAVATED MYOTONIA MET-445.
RX   PubMed=9392583;
RA   Rosenfeld J., Sloan-Brown K., George A.L. Jr.;
RT   "A novel muscle sodium channel mutation causes painful congenital
RT   myotonia.";
RL   Ann. Neurol. 42:811-814(1997).
RN   [16]
RP   VARIANT POTASSIUM-AGGRAVATED MYOTONIA MET-445.
RX   PubMed=10218481;
RA   Wang D.W., VanDeCarr D., Ruben P.C., George A.L. Jr., Bennett P.B.;
RT   "Functional consequences of a domain 1/S6 segment sodium channel
RT   mutation associated with painful congenital myotonia.";
RL   FEBS Lett. 448:231-234(1999).
RN   [17]
RP   VARIANT HYPOKPP HIS-669.
RX   PubMed=10599760;
RA   Bulman D.E., Scoggan K.A., van Oene M.D., Nicolle M.W., Hahn A.F.,
RA   Tollar L.L., Ebers G.C.;
RT   "A novel sodium channel mutation in a family with hypokalemic periodic
RT   paralysis.";
RL   Neurology 53:1932-1936(1999).
RN   [18]
RP   VARIANT HYPOKPP SER-1158.
RX   PubMed=10851391;
RA   Sugiura Y., Aoki T., Sugiyama Y., Hida C., Ogata M., Yamamoto T.;
RT   "Temperature-sensitive sodium channelopathy with heat-induced myotonia
RT   and cold-induced paralysis.";
RL   Neurology 54:2179-2181(2000).
RN   [19]
RP   VARIANTS HYPOKPP GLY-672 AND HIS-672.
RX   PubMed=10944223;
RA   Jurkat-Rott K., Mitrovic N., Hang C., Kouzmekine A., Iaizzo P.,
RA   Herzog J., Lerche H., Nicole S., Vale-Santos J., Chauveau D.,
RA   Fontaine B., Lehmann-Horn F.;
RT   "Voltage-sensor sodium channel mutations cause hypokalemic periodic
RT   paralysis type 2 by enhanced inactivation and reduced current.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:9549-9554(2000).
RN   [20]
RP   VARIANT HYPOKPP SER-672.
RX   PubMed=11558801;
RA   Bendahhou S., Cummins T.R., Griggs R.C., Fu Y.H., Ptacek L.J.;
RT   "Sodium channel inactivation defects are associated with
RT   acetazolamide-exacerbated hypokalemic periodic paralysis.";
RL   Ann. Neurol. 50:417-420(2001).
RN   [21]
RP   VARIANT HYPOKPP SER-672.
RX   PubMed=11591859;
RA   Davies N.P., Eunson L.H., Samuel M., Hanna M.G.;
RT   "Sodium channel gene mutations in hypokalemic periodic paralysis: an
RT   uncommon cause in the UK.";
RL   Neurology 57:1323-1325(2001).
CC   -!- FUNCTION: This protein mediates the voltage-dependent sodium ion
CC       permeability of excitable membranes. Assuming opened or closed
CC       conformations in response to the voltage difference across the
CC       membrane, the protein forms a sodium-selective channel through
CC       which Na+ ions may pass in accordance with their electrochemical
CC       gradient. This sodium channel may be present in both denervated
CC       and innervated skeletal muscle.
CC   -!- SUBUNIT: Muscle sodium channels contain an alpha subunit and a
CC       smaller beta subunit. Interacts with the PDZ domain of the
CC       syntrophin SNTA1, SNTB1 and SNTB2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- DISEASE: Defects in SCN4A are the cause of paramyotonia congenita
CC       of von Eulenburg (PMC) [MIM:168300]. PMC is an autosomal dominant
CC       sodium channel disease characterized by myotonia, increased by
CC       exposure to cold, intermittent flaccid paresis, not necessarily

  Query Match             71.4%;  Score 20;  DB 1;  Length 1836;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 IFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||
Db        431 IFLGSFYLINLILAVVAMAY 450


RESULT 18
CIN4_RAT
ID   CIN4_RAT       STANDARD;      PRT;  1840 AA.
AC   P15390;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type IV alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.4) (Sodium channel protein, skeletal muscle
DE   alpha-subunit) (Mu-1).
GN   Name=Scn4a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90148778; PubMed=2559760;
RA   Trimmer J.S., Cooperman S.S., Tomiko S.A., Zhou J., Crean S.M.,
RA   Boyle M.B., Kallen R.G., Sheng Z., Barchi R.L., Sigworth F.J.,
RA   Goodman R.H., Agnew W.S., Mandel G.;
RT   "Primary structure and functional expression of a mammalian skeletal
RT   muscle sodium channel.";
RL   Neuron 3:33-49(1989).
CC   -!- FUNCTION: This protein mediates the voltage-dependent sodium ion
CC       permeability of excitable membranes. Assuming opened or closed
CC       conformations in response to the voltage difference across the
CC       membrane, the protein forms a sodium-selective channel through
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CC       which Na+ ions may pass in accordance with their electrochemical
CC       gradient. This sodium channel may be present in both denervated
CC       and innervated skeletal muscle.
CC   -!- SUBUNIT: Muscle sodium channels contain an alpha subunit and a
CC       smaller beta subunit. Interacts with the PDZ domain of the
CC       syntrophin SNTA1, SNTB1 and SNTB2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M26643; AAA41682.1; -.
DR   PIR; JN0007; CHRTM1.
DR   HSSP; P04775; 1BYY.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008052; Na_channel4.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01665; NACHANNEL4.
DR   PROSITE; PS50096; IQ; 1.
KW   Glycoprotein; Ion transport; Ionic channel; Multigene family;
KW   Phosphorylation; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   TRANSMEM    130    152       S1 of repeat I.
FT   TRANSMEM    156    179       S2 of repeat I.
FT   TRANSMEM    192    212       S3 of repeat I.
FT   TRANSMEM    214    233       S4 of repeat I.
FT   TRANSMEM    252    274       S5 of repeat I.
FT   TRANSMEM    417    444       S6 of repeat I.
FT   TRANSMEM    571    593       S1 of repeat II.
FT   TRANSMEM    663    685       S2 of repeat II.
FT   TRANSMEM    696    721       S3 of repeat II.
FT   TRANSMEM    722    737       S4 of repeat II.
FT   TRANSMEM    756    778       S5 of repeat II.
FT   TRANSMEM    832    859       S6 of repeat II.
FT   TRANSMEM   1084   1105       S1 of repeat III.
FT   TRANSMEM   1117   1140       S2 of repeat III.
FT   TRANSMEM   1149   1168       S3 of repeat III.
FT   TRANSMEM   1176   1195       S4 of repeat III.
FT   TRANSMEM   1215   1236       S5 of repeat III.
FT   TRANSMEM   1324   1351       S6 of repeat III.
FT   TRANSMEM   1405   1427       S1 of repeat IV.
FT   TRANSMEM   1437   1460       S2 of repeat IV.
FT   TRANSMEM   1468   1487       S3 of repeat IV.
FT   TRANSMEM   1502   1522       S4 of repeat IV.
FT   TRANSMEM   1535   1556       S5 of repeat IV.
FT   TRANSMEM   1627   1653       S6 of repeat IV.
FT   DOMAIN     1720   1749       IQ.
FT   CARBOHYD    288    288       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    291    291       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    297    297       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    303    303       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    309    309       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    315    315       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    327    327       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    356    356       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    502    502       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    954    954       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1198   1198       N-linked (GlcNAc. . .) (Potential).
FT   MOD_RES      56     56       Phosphoserine (by PKA) (Potential).
FT   MOD_RES     251    251       Phosphoserine (by PKA) (Potential).
FT   MOD_RES    1321   1321       Phosphoserine (by PKA) (Potential).
FT   MOD_RES    1504   1504       Phosphoserine (by PKA) (Potential).
SQ   SEQUENCE   1840 AA;  208865 MW;  C5DC09D93DD9FAD6 CRC64;
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  Query Match           71.4%;  Score 20;  DB 1;  Length 1840;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 IFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||
Db        425 IFLGSFYLINLILAVVAMAY 444
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RESULT 19
O70611
ID   O70611      PRELIMINARY;      PRT;  1840 AA.
AC   O70611;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Rat skeletal muscle type 1 voltage-gated sodium channel (RSkM1)
DE   variant.
GN   Name=SCN4A;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Copenhagen; TISSUE=Prostate;
RX   MEDLINE=98273645; PubMed=9613589;
RA   Diss J.K.J., Stewart D., Fraser S.P., Black J.A., Dibb-Hajj S.,
RA   Waxman S.G., Archer S.N., Djamgoz M.B.A.;
RT   "Expression of skeletal muscle-type voltage-gated Na+ channel in rat
RT   and human prostate cancer cell lines.";
RL   FEBS Lett. 427:5-10(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; Y17153; CAA76659.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008052; Na_channel4.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01665; NACHANNEL4.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1840 AA;  208823 MW;  B1DFFA538E264B40 CRC64;
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  Query Match           71.4%;  Score 20;  DB 2;  Length 1840;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 IFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||
Db        425 IFLGSFYLINLILAVVAMAY 444


RESULT 20
Q9ER60
ID   Q9ER60      PRELIMINARY;      PRT;  1841 AA.
AC   Q9ER60;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel.
GN   Name=Scn4a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=balb/c; TISSUE=Heart;
RX   MEDLINE=21823196; PubMed=11834499;
RA   Zimmer T., Benndorf K.;
RT   "The mouse heart sodium channel (mH1): cloning and characterization of
RT   alternatively spliced variants.";
RL   Am. J. Physiol. Heart Circ. Physiol. 282:H1007-H1017(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AJ278787; CAC17146.1; -.
DR   HSSP; P04775; 1BYY.
DR   MGD; MGI:98250; Scn4a.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008052; Na_channel4.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01665; NACHANNEL4.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1841 AA;  208796 MW;  0766DFD33A9E0E55 CRC64;

  Query Match           71.4%;  Score 20;  DB 2;  Length 1841;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 IFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||
Db        425 IFLGSFYLINLILAVVAMAY 444


RESULT 21
Q90518
ID   Q90518      PRELIMINARY;      PRT;  530 AA.
AC   Q90518;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Sodium channel alpha subunit (Fragment).
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Nakazawa A.;
RL   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; D37976; BAA07194.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER     530     530
SQ   SEQUENCE   530 AA;  60164 MW;  2F9AE902C8F74071 CRC64;

  Query Match           57.1%;  Score 16;  DB 2;  Length 530;
  Best Local Similarity  100.0%;  Pred. No. 6.2e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYL 16
              ||||||||||||||||
Db        392 YMIFFVLVIFLGSFYL 407


RESULT 22
Q803T8
ID   Q803T8      PRELIMINARY;      PRT;  711 AA.
AC   Q803T8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to sodium channel, voltage-gated, type 1, alpha
DE   polypeptide.
GN   Name=zgc:55600;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AB; TISSUE=Whole body;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
```

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RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AB; TISSUE=Whole body;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC044197; AAH44197.1; -.
DR   HSSP; P08104; 1QG9.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
SQ   SEQUENCE   711 AA;  80547 MW;  0BDE497E3BF85033 CRC64;

  Query Match             57.1%;  Score 16;  DB 2;  Length 711;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYL 16
              ||||||||||||||||
Db        382 YMIFFVLVIFLGSFYL 397


RESULT 23
Q28371
ID   Q28371      PRELIMINARY;      PRT;  1834 AA.
AC   Q28371;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Skeletal muscle sodium channel alpha-subunit.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle plasma membrane;
RA   Stephan D.A., Wang J., Spier S., Hoffman E.P.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; U25990; AAA67366.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008052; Na_channel4.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01665; NACHANNEL4.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
DR   PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1834 AA;  207485 MW;  01D62B25CD577D97 CRC64;

  Query Match             57.1%;  Score 16;  DB 2;  Length 1834;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 IFLGSFYLINLILAVV 24
              ||||||||||||||||
Db        425 IFLGSFYLINLILAVV 440


RESULT 24
CIN3_RAT
ID   CIN3_RAT       STANDARD;      PRT;  1951 AA.
AC   P08104;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Sodium channel protein type III alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.3) (Sodium channel protein, brain III alpha
DE   subunit) (Voltage-gated sodium channel subtype III).
GN   Name=Scn3a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar;
RX   MEDLINE=88137594; PubMed=2449363;
RA   Kayano T., Noda M., Flockerzi V., Takahashi H., Numa S.;
RT   "Primary structure of rat brain sodium channel III deduced from the
RT   cDNA sequence.";
RL   FEBS Lett. 228:187-194(1988).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y00766; CAA68735.1; -.
DR   PIR; S00320; S00320.
DR   PDB; 1QG9; NMR; A=156-176.
DR   RGD; 3635; Scn3a.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
```

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DR   PROSITE; PS50096; IQ; FALSE_NEG.
KW   3D-structure; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   REPEAT      110    455       I.
FT   REPEAT      693    965       II.
FT   REPEAT     1139   1450       III.
FT   REPEAT     1459   1757       IV.
FT   TRANSMEM    124    147       S1 of repeat I.
FT   TRANSMEM    156    175       S2 of repeat I.
FT   TRANSMEM    189    207       S3 of repeat I.
FT   TRANSMEM    214    233       S4 of repeat I.
FT   TRANSMEM    249    273       S5 of repeat I.
FT   TRANSMEM    401    426       S6 of repeat I.
FT   TRANSMEM    706    730       S1 of repeat II.
FT   TRANSMEM    742    765       S2 of repeat II.
FT   TRANSMEM    774    793       S3 of repeat II.
FT   TRANSMEM    800    820       S4 of repeat II.
FT   TRANSMEM    836    856       S5 of repeat II.
FT   TRANSMEM    910    935       S6 of repeat II.
FT   TRANSMEM   1153   1176       S1 of repeat III.
FT   TRANSMEM   1190   1215       S2 of repeat III.
FT   TRANSMEM   1222   1243       S3 of repeat III.
FT   TRANSMEM   1248   1269       S4 of repeat III.
FT   TRANSMEM   1289   1310       S5 of repeat III.
FT   TRANSMEM   1393   1419       S6 of repeat III.
FT   TRANSMEM   1473   1496       S1 of repeat IV.
FT   TRANSMEM   1508   1531       S2 of repeat IV.
FT   TRANSMEM   1538   1561       S3 of repeat IV.
FT   TRANSMEM   1572   1593       S4 of repeat IV.
FT   TRANSMEM   1609   1631       S5 of repeat IV.
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FT   CARBOHYD    290    290       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    296    296       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    302    302       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    307    307       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    339    339       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    624    624       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    835    835       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1002   1002       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1019   1019       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1085   1085       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1317   1317       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1331   1331       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   1951 AA;  221385 MW;  74E5E851524BD10E CRC64;
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Db        400 YMIFFVLVIFLGSFYL 415
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DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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GN   Name=SCN3A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jeong S.-Y., Goto J., Kanazawa I.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AF225986; AAK00218.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1951 AA;  221517 MW;  99AD4C032CE124AB CRC64;
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Qy          1 YMIFFVLVIFLGSFYL 16
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Db        400 YMIFFVLVIFLGSFYL 415
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Job time : 96.5 secs
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:36:50 ; Search time 22.5 Seconds
(without alignments)
82.529 Million cell updates/sec

Title: US-10-608-584-1
Perfect score: 28
Sequence: 1 YMIFFVLVIFLGSFYLINLILAVVAMAY 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	28	100.0	2005	4	US-09-457-571-7	Sequence 7, Appli
3	21	75.0	1835	3	US-08-836-325-15	Sequence 15, Appl
4	21	75.0	1835	4	US-09-457-571-15	Sequence 15, Appl
5	21	75.0	1969	3	US-08-836-325-16	Sequence 16, Appl
6	21	75.0	1969	4	US-09-457-571-16	Sequence 16, Appl
7	21	75.0	1977	4	US-09-976-594-757	Sequence 757, App
8	21	75.0	1977	4	US-09-919-039-367	Sequence 367, App
9	21	75.0	1984	3	US-08-836-325-10	Sequence 10, Appl
10	21	75.0	1984	4	US-09-457-571-10	Sequence 10, Appl
11	21	75.0	1989	3	US-08-836-325-11	Sequence 11, Appl
12	21	75.0	1989	3	US-08-836-325-12	Sequence 12, Appl
13	21	75.0	1989	4	US-09-457-571-11	Sequence 11, Appl
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15	20	71.4	1836	4	US-10-162-012-24	Sequence 24, Appl
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17	16	57.1	1956	3	US-08-843-417-10	Sequence 10, Appl
18	16	57.1	1956	4	US-09-527-013-10	Sequence 10, Appl
19	13	46.4	1956	3	US-08-843-417-2	Sequence 2, Appli
20	13	46.4	1956	4	US-09-527-013-2	Sequence 2, Appli
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23	13	46.4	2132	4	US-08-669-656A-6	Sequence 6, Appli
24	12	42.9	1024	4	US-09-562-737-83	Sequence 83, Appl
25	12	42.9	1233	4	US-09-354-147C-7	Sequence 7, Appli
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29	11	39.3	1976	3	US-09-425-043-9	Sequence 9, Appli
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31	11	39.3	1978	3	US-09-425-043-3	Sequence 3, Appli
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35	11	39.3	2016	4	US-09-514-907A-2	Sequence 2, Appli
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38	9	32.1	1024	4	US-09-562-737-82	Sequence 82, Appl
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59	6	21.4	43	1	US-08-118-270-310	Sequence 310, App
60	6	21.4	43	5	PCT-US93-08528-310	Sequence 310, App
61	6	21.4	44	1	US-08-118-270-312	Sequence 312, App
62	6	21.4	44	5	PCT-US93-08528-312	Sequence 312, App
63	6	21.4	46	1	US-08-118-270-313	Sequence 313, App
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66	6	21.4	48	5	PCT-US93-08528-314	Sequence 314, App
67	6	21.4	82	4	US-09-134-000C-5571	Sequence 5571, Ap
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81	6	21.4	147	4	US-09-270-767-38096	Sequence 38096, A
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92	6	21.4	208	3	US-08-718-904-7	Sequence 7, Appli
93	6	21.4	208	3	US-09-181-974-2	Sequence 2, Appli
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ALIGNMENTS

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RESULT 1
US-08-836-325-7
; Sequence 7, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2005 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-836-325-7

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Db        401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428


RESULT 2
US-09-457-571-7
; Sequence 7, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-457-571-7

  Query Match             100.0%;  Score 28;  DB 4;  Length 2005;
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Db        401 YMIFFVLVIFLGSFYLINLILAVVAMAY 428


RESULT 3
US-08-836-325-15
; Sequence 15, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
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;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1835 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-836-325-15

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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        363 VIFLGSFYLINLILAVVAMAY 383


RESULT 4
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; Sequence 15, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1835 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-09-457-571-15

  Query Match             75.0%;  Score 21;  DB 4;  Length 1835;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        363 VIFLGSFYLINLILAVVAMAY 383


RESULT 5
US-08-836-325-16
; Sequence 16, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  US/08/836,325
;       FILING DATE:  2-MAY-1997
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/14251
;       FILING DATE:  02-NOV-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/482,401
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/334,029
;       FILING DATE:  02-NOV-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ludwig, Steven R.
;       REGISTRATION NUMBER:  36,203
;       REFERENCE/DOCKET NUMBER:  0917.0240002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  16:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1969 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-836-325-16

  Query Match             75.0%;  Score 21;  DB 3;  Length 1969;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        385 VIFLGSFYLINLILAVVAMAY 405


RESULT 6
US-09-457-571-16
; Sequence 16, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1969 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-457-571-16

  Query Match             75.0%;  Score 21;  DB 4;  Length 1969;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        385 VIFLGSFYLINLILAVVAMAY 405


RESULT 7
US-09-976-594-757
; Sequence 757, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 757
;   LENGTH: 1977
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 1719478CD1
US-09-976-594-757

  Query Match             75.0%;  Score 21;  DB 4;  Length 1977;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        385 VIFLGSFYLINLILAVVAMAY 405


RESULT 8
US-09-919-039-367
; Sequence 367, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
;  APPLICANT: Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;  FILE REFERENCE: PA-0035 US
;  CURRENT APPLICATION NUMBER: US/09/919,039
;  CURRENT FILING DATE:  2002-09-09
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;  PRIOR APPLICATION NUMBER: 60/222,113
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 401
;  SOFTWARE: PERL Program
; SEQ ID NO 367
;   LENGTH: 1977
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6727066 1719478CD1
US-09-919-039-367

  Query Match             75.0%;  Score 21;  DB 4;  Length 1977;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        385 VIFLGSFYLINLILAVVAMAY 405


RESULT 9
US-08-836-325-10
; Sequence 10, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1984 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-836-325-10

  Query Match             75.0%;  Score 21;  DB 3;  Length 1984;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        385 VIFLGSFYLINLILAVVAMAY 405


RESULT 10
US-09-457-571-10
; Sequence 10, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1984 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-457-571-10

  Query Match             75.0%;  Score 21;  DB 4;  Length 1984;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
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                     ||||||||||||||||||||
Db        385 VIFLGSFYLINLILAVVAMAY 405


RESULT 11
US-08-836-325-11
; Sequence 11, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1989 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-836-325-11

  Query Match             75.0%;  Score 21;  DB 3;  Length 1989;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||
Db        385 VIFLGSFYLINLILAVVAMAY 405


RESULT 12
US-08-836-325-12
; Sequence 12, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1989 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-836-325-12

  Query Match             75.0%;  Score 21;  DB 3;  Length 1989;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||
Db        385 VIFLGSFYLINLILAVVAMAY 405


RESULT 13
US-09-457-571-11
; Sequence 11, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;       STREET:  1100 New York Ave., N. W., Suite 600
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20005-3934
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/457,571
;       FILING DATE:  09-DEC-1999
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/836,325
;       FILING DATE:  02-MAY-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/14251
;       FILING DATE:  02-NOV-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/482,401
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/334,029
;       FILING DATE:  02-NOV-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ludwig, Steven R.
;       REGISTRATION NUMBER:  36,203
;       REFERENCE/DOCKET NUMBER:  0917.0240003
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1989 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  protein
US-09-457-571-11

  Query Match             75.0%;  Score 21;  DB 4;  Length 1989;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        385 VIFLGSFYLINLILAVVAMAY 405


RESULT 14
US-09-457-571-12
; Sequence 12, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;     APPLICANT:  Mandel, Gail
;     APPLICANT:  Halegoua, Simon
;     TITLE OF INVENTION:  Peripheral Nervous System Specific
;     TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;     TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;     TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;     TITLE OF INVENTION:  Thereof
;     NUMBER OF SEQUENCES:  19
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;       STREET:  1100 New York Ave., N. W., Suite 600
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20005-3934
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/457,571
;       FILING DATE:  09-DEC-1999
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/836,325
;       FILING DATE:  02-MAY-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/14251
;       FILING DATE:  02-NOV-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/482,401
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/334,029
;       FILING DATE:  02-NOV-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ludwig, Steven R.
;       REGISTRATION NUMBER:  36,203
;       REFERENCE/DOCKET NUMBER:  0917.0240003
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1989 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  protein
US-09-457-571-12

  Query Match             75.0%;  Score 21;  DB 4;  Length 1989;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINLILAVVAMAY 28
              |||||||||||||||||||||
Db        385 VIFLGSFYLINLILAVVAMAY 405


RESULT 15
US-10-162-012-24
; Sequence 24, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  Gu, Wei
;  TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
;  FILE REFERENCE: 10448-190001
;  CURRENT APPLICATION NUMBER: US/10/162,012
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: US 60/209,845
;  PRIOR FILING DATE: 2000-06-06
;  PRIOR APPLICATION NUMBER: US 09/875,321
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: PCT/US01/18340
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/209,257
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,423
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18398
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/209,238
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,363
;  PRIOR FILING DATE: 2001-06-05
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;  PRIOR APPLICATION NUMBER: PCT/US01/18247
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/227,068
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: US 09/928,530
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: PCT/US01/25475
;  PRIOR FILING DATE: 2001-08-15
;  PRIOR APPLICATION NUMBER: US 60/226,770
;  PRIOR FILING DATE: 2000-08-21
;  PRIOR APPLICATION NUMBER: US 09/934,421
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: PCT/US01/26096
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: US 60/279,281
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 10/109,029
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: PCT/US02/09728
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 60/290,288
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US (not assigned)
;  PRIOR FILING DATE: 2002-05-13
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 1836
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-162-012-24

  Query Match             71.4%;  Score 20;  DB 4;  Length 1836;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 IFLGSFYLINLILAVVAMAY 28
              ||||||||||||||||||||
Db        431 IFLGSFYLINLILAVVAMAY 450


RESULT 16
US-09-562-737-81
; Sequence 81, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
;  APPLICANT:  Herz, Joachim
;  APPLICANT:  Gotthardt, Michael
;  TITLE OF INVENTION:  LDL Receptor Signaling Pathways
;  FILE REFERENCE:  UTSW0708
;  CURRENT APPLICATION NUMBER: US/09/562,737
;  CURRENT FILING DATE:  2000-05-01
;  NUMBER OF SEQ ID NOS:  132
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 1024
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Sequence
US-09-562-737-81

  Query Match             57.1%;  Score 16;  DB 4;  Length 1024;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYL 16
              ||||||||||||||||
Db        400 YMIFFVLVIFLGSFYL 415


RESULT 17
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```
US-08-843-417-10
; Sequence 10, Application US/08843417
; Patent No. 6184349
;  GENERAL INFORMATION:
;    APPLICANT:  Herman, Ronald C
;    APPLICANT:  Delgado, Stephen G
;    APPLICANT:  Fish, Linda M
;    APPLICANT:  Sangameswaran, Lakshmi
;    APPLICANT:  Rabert, Douglas K
;    TITLE OF INVENTION:  CLONED PERIPHERAL NERVE
;    TITLE OF INVENTION:  TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Heller Ehrman White & McAuliffe
;      STREET:  525 University Ave
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/843,417
;      FILING DATE:  April 15, 1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Schmonsees, William
;      REGISTRATION NUMBER:  31,796
;      REFERENCE/DOCKET NUMBER:  28340-P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415)-324-7041
;      TELEFAX:  (415)-324-0638
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1956 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-843-417-10

  Query Match             57.1%;  Score 16;  DB 3;  Length 1956;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYL 16
              ||||||||||||||||
Db        373 YMIFFVLVIFLGSFYL 388


RESULT 18
US-09-527-013-10
; Sequence 10, Application US/09527013
; Patent No. 6479259
;  GENERAL INFORMATION:
;       APPLICANT: Herman, Ronald C
;                  Delgado, Stephen G
;                  Fish, Linda M
;                  Sangameswaran, Lakshmi
;                  Rabert, Douglas K
;       TITLE OF INVENTION: CLONED PERIPHERAL NERVE
;                           TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
;       NUMBER OF SEQUENCES: 10
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Heller Ehrman White & McAuliffe
;            STREET: 525 University Ave
;            CITY: Palo Alto
;            STATE: CA
```

```
;            COUNTRY: U.S.A.
;            ZIP: 94301
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/527,013
;            FILING DATE: 16-Mar-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/843,417
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Schmonsees, William
;            REGISTRATION NUMBER: 31,796
;            REFERENCE/DOCKET NUMBER: 28340-P1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415)-324-7041
;            TELEFAX: (415)-324-0638
;  INFORMATION FOR SEQ ID NO: 10:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1956 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: unknown
;            TOPOLOGY: unknown
;       MOLECULE TYPE: peptide
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-527-013-10

  Query Match             57.1%;  Score 16;  DB 4;  Length 1956;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YMIFFVLVIFLGSFYL 16
              ||||||||||||||||
Db        373 YMIFFVLVIFLGSFYL 388


RESULT 19
US-08-843-417-2
; Sequence 2, Application US/08843417
; Patent No. 6184349
;  GENERAL INFORMATION:
;    APPLICANT:  Herman, Ronald C
;    APPLICANT:  Delgado, Stephen G
;    APPLICANT:  Fish, Linda M
;    APPLICANT:  Sangameswaran, Lakshmi
;    APPLICANT:  Rabert, Douglas K
;    TITLE OF INVENTION:  CLONED PERIPHERAL NERVE
;    TITLE OF INVENTION:  TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Heller Ehrman White & McAuliffe
;      STREET:  525 University Ave
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/843,417
;      FILING DATE:  April 15, 1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Schmonsees, William
;      REGISTRATION NUMBER:  31,796
;      REFERENCE/DOCKET NUMBER:  28340-P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415)-324-7041
;      TELEFAX:  (415)-324-0638
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1956 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ORIGINAL SOURCE:
;      ORGANISM:  rat
;      TISSUE TYPE:  dorsal root ganglia
;      CELL TYPE:  peripheral nerve
US-08-843-417-2

  Query Match             46.4%;  Score 13;  DB 3;  Length 1956;
  Best Local Similarity   100.0%;  Pred. No. 0.00012;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 FFVLVIFLGSFYL 16
              |||||||||||||
Db        375 FFVLVIFLGSFYL 387


RESULT 20
US-09-527-013-2
; Sequence 2, Application US/09527013
; Patent No. 6479259
;  GENERAL INFORMATION:
;       APPLICANT: Herman, Ronald C
;                  Delgado, Stephen G
;                  Fish, Linda M
;                  Sangameswaran, Lakshmi
;                  Rabert, Douglas K
;       TITLE OF INVENTION: CLONED PERIPHERAL NERVE
;                           TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
;       NUMBER OF SEQUENCES: 10
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Heller Ehrman White & McAuliffe
;            STREET: 525 University Ave
;            CITY: Palo Alto
;            STATE: CA
;            COUNTRY: U.S.A.
;            ZIP: 94301
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/527,013
;            FILING DATE: 16-Mar-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/843,417
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Schmonsees, William
;            REGISTRATION NUMBER: 31,796
;            REFERENCE/DOCKET NUMBER: 28340-P1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415)-324-7041
;            TELEFAX: (415)-324-0638
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1956 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: not relevant
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```
;        MOLECULE TYPE: protein
;        HYPOTHETICAL: YES
;        ORIGINAL SOURCE:
;             ORGANISM: rat
;             TISSUE TYPE: dorsal root ganglia
;             CELL TYPE: peripheral nerve
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-527-013-2

  Query Match             46.4%;  Score 13;  DB 4;  Length 1956;
  Best Local Similarity   100.0%;  Pred. No. 0.00012;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 FFVLVIFLGSFYL 16
              |||||||||||||
Db        375 FFVLVIFLGSFYL 387


RESULT 21
US-08-669-656A-2
; Sequence 2, Application US/08669656A
; Patent No. 6451554
;  GENERAL INFORMATION:
;    APPLICANT:  Wood, John N.
;    APPLICANT:  Akopian, Armen N.
;    TITLE OF INVENTION:  Ion Channel
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZENECA Pharmaceuticals
;      STREET:  1800 Concord Pike, P.O. Box 15437
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/669,656A
;      FILING DATE:  24-JUN-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hohenschutz, Liza D.
;      REGISTRATION NUMBER:  33,712
;      REFERENCE/DOCKET NUMBER:  PHM.70086
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (302) 886-7466
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1957 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-669-656A-2

  Query Match             46.4%;  Score 13;  DB 4;  Length 1957;
  Best Local Similarity   100.0%;  Pred. No. 0.00012;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 FFVLVIFLGSFYL 16
              |||||||||||||
Db        375 FFVLVIFLGSFYL 387


RESULT 22
US-08-669-656A-8
; Sequence 8, Application US/08669656A
; Patent No. 6451554
;  GENERAL INFORMATION:
;    APPLICANT:  Wood, John N.
;    APPLICANT:  Akopian, Armen N.
;    TITLE OF INVENTION:  Ion Channel
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZENECA Pharmaceuticals
;      STREET:  1800 Concord Pike, P.O. Box 15437
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/669,656A
;      FILING DATE:  24-JUN-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hohenschutz, Liza D.
;      REGISTRATION NUMBER:  33,712
;      REFERENCE/DOCKET NUMBER:  PHM.70086
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (302) 886-7466
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1957 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-669-656A-8

  Query Match             46.4%;  Score 13;  DB 4;  Length 1957;
  Best Local Similarity   100.0%;  Pred. No. 0.00012;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 FFVLVIFLGSFYL 16
              |||||||||||||
Db        375 FFVLVIFLGSFYL 387


RESULT 23
US-08-669-656A-6
; Sequence 6, Application US/08669656A
; Patent No. 6451554
;  GENERAL INFORMATION:
;    APPLICANT:  Wood, John N.
;    APPLICANT:  Akopian, Armen N.
;    TITLE OF INVENTION:  Ion Channel
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZENECA Pharmaceuticals
;      STREET:  1800 Concord Pike, P.O. Box 15437
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/669,656A
;      FILING DATE:  24-JUN-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hohenschutz, Liza D.
;      REGISTRATION NUMBER:  33,712
;      REFERENCE/DOCKET NUMBER:  PHM.70086
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (302) 886-7466
;  INFORMATION FOR SEQ ID NO:  6:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2132 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-669-656A-6

  Query Match             46.4%;  Score 13;  DB 4;  Length 2132;
  Best Local Similarity   100.0%;  Pred. No. 0.00013;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 FFVLVIFLGSFYL 16
              |||||||||||||
Db        375 FFVLVIFLGSFYL 387


RESULT 24
US-09-562-737-83
; Sequence 83, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
;  APPLICANT:  Herz, Joachim
;  APPLICANT:  Gotthardt, Michael
;  TITLE OF INVENTION:  LDL Receptor Signaling Pathways
;  FILE REFERENCE:  UTSW0708
;  CURRENT APPLICATION NUMBER: US/09/562,737
;  CURRENT FILING DATE:  2000-05-01
;  NUMBER OF SEQ ID NOS:  132
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 83
;   LENGTH: 1024
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Sequence
US-09-562-737-83

  Query Match             42.9%;  Score 12;  DB 4;  Length 1024;
  Best Local Similarity   100.0%;  Pred. No. 0.00066;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVLVIFLGSFYL 16
              ||||||||||||
Db        404 FVLVIFLGSFYL 415


RESULT 25
US-09-354-147C-7
; Sequence 7, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
;  APPLICANT: Dib-Hajj, Sulayman
;  APPLICANT:  Waxman, Stephen G.
;  TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
;  FILE REFERENCE: 44574-5004-01-US
;  CURRENT APPLICATION NUMBER: US/09/354,147C
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER: US 60/072,990
;  PRIOR FILING DATE: 1998-01-29
;  PRIOR APPLICATION NUMBER: US 60/109,402
;  PRIOR FILING DATE: 1998-11-20
;  PRIOR APPLICATION NUMBER: PCT/US99/02008
;  PRIOR FILING DATE: 1999-01-29
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 1233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: (308)
;   OTHER INFORMATION: Xaa is Leu. Xaa results from a "y" in SEQ ID NO: 6.
US-09-354-147C-7

  Query Match             42.9%;  Score 12;  DB 4;  Length 1233;
  Best Local Similarity   100.0%;  Pred. No. 0.00078;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VIFLGSFYLINL 19
              ||||||||||||
Db        184 VIFLGSFYLINL 195


Search completed: January 27, 2005, 17:54:17
Job time : 23.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:32:04 ; Search time 86.5 Seconds
(without alignments)
116.120 Million cell updates/sec

Title: US-10-608-584-13
Perfect score: 28
Sequence: 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	100.0	1795	7	ADB78596	Adb78596 Human sod
2	28	100.0	1855	7	ADB78597	Adb78597 Human sod
3	28	100.0	1981	7	ABR83185	Abr83185 Human SCN
4	28	100.0	1998	7	ABR83184	Abr83184 Human SCN
5	28	100.0	1999	5	ABB06026	Abb06026 Human sod
6	28	100.0	2005	4	AAB99676	Aab99676 Human adu
7	28	100.0	2005	4	AAB99677	Aab99677 Human neo
8	28	100.0	2005	5	ABB83627	Abb83627 Human GEF
9	28	100.0	2005	7	ADB78604	Adb78604 Human sod
10	28	100.0	2005	7	ADB78603	Adb78603 Human sod
11	28	100.0	2005	7	ADB78605	Adb78605 Human sod
12	28	100.0	2005	7	ADC46947	Adc46947 Human SCN
13	28	100.0	2009	4	AAB99674	Aab99674 Human adu
14	28	100.0	2009	5	ABG69292	Abg69292 Human sod
15	28	100.0	2009	5	ABG69291	Abg69291 Human sod
16	28	100.0	2009	5	ABG69293	Abg69293 Human sod
17	28	100.0	2009	5	ABG69289	Abg69289 Human sod
18	28	100.0	2009	5	ABG69290	Abg69290 Human sod
19	28	100.0	2009	5	ABB83626	Abb83626 Human GEF
20	28	100.0	2009	5	AAE16776	Aae16776 Human tra
21	28	100.0	2009	7	ADB78599	Adb78599 Human sod
22	28	100.0	2009	7	ADB78595	Adb78595 Human sod
23	28	100.0	2009	7	ADB78593	Adb78593 Human sod
24	28	100.0	2009	7	ADB78594	Adb78594 Human sod
25	28	100.0	2009	7	ADB78598	Adb78598 Human sod
26	28	100.0	2009	7	ABR83180	Abr83180 Human SCN
27	28	100.0	2009	7	ADE57563	Ade57563 Human Pro
28	25	89.3	1976	7	ADE57386	Ade57386 Rat Prote
29	25	89.3	1978	2	AAW69361	Aaw69361 Tetrodoto
30	25	89.3	1980	3	AAB23563	Aab23563 Human sod
31	25	89.3	1980	5	AAO14927	Aao14927 Human sod
32	25	89.3	1980	7	ADB78600	Adb78600 Human sod
33	25	89.3	1980	7	ADB78606	Adb78606 Human sod
34	25	89.3	1988	2	AAW69362	Aaw69362 Tetrodoto
35	24	85.7	1381	5	AAE20513	Aae20513 Human ion
36	24	85.7	1387	5	AAE20514	Aae20514 Human ion
37	24	85.7	1392	5	AAE20518	Aae20518 Human ion
38	24	85.7	1398	5	AAE20519	Aae20519 Human ion
39	24	85.7	1442	5	AAE20512	Aae20512 Human ion
40	24	85.7	1453	5	AAE20517	Aae20517 Human ion
41	24	85.7	1962	5	AAE20511	Aae20511 Human ion
42	24	85.7	1973	5	AAE20516	Aae20516 Human ion
43	24	85.7	1998	5	AAE20510	Aae20510 Human ion
44	24	85.7	2009	5	AAE20515	Aae20515 Human ion
45	23	82.1	1835	2	AAR92316	Aar92316 Periphera
46	23	82.1	1977	2	AAR99641	Aar99641 Periphera
47	23	82.1	1977	8	ADE77202	Ade77202 Human pro
48	23	82.1	1977	8	ADL13028	Adl13028 Human ste
49	23	82.1	1978	7	ADE54553	Ade54553 Human Pro
50	23	82.1	1978	7	ADE54549	Ade54549 Human Pro
51	23	82.1	1984	2	AAR99639	Aar99639 Periphera
52	23	82.1	1984	7	ADE54547	Ade54547 Rat Prote
53	23	82.1	1984	7	ADE54551	Ade54551 Rat Prote
54	23	82.1	1984	7	ADE63027	Ade63027 Rat Prote
55	23	82.1	1989	2	AAR92317	Aar92317 Periphera
56	23	82.1	1989	2	AAR99640	Aar99640 Periphera
57	22	78.6	1836	7	ADE57388	Ade57388 Human Pro
58	22	78.6	1836	7	ADE59630	Ade59630 Human Pro
59	22	78.6	1836	7	ADE63029	Ade63029 Human Pro
60	22	78.6	1836	8	ADQ17412	Adq17412 Human sof
61	21	75.0	1024	5	ABB04858	Abb04858 LDL recep
62	21	75.0	1107	6	ABR41495	Abr41495 Human DIT
63	21	75.0	1366	7	ADJ68488	Adj68488 Human hea
64	21	75.0	1366	8	ADL06575	Adl06575 Human tum
65	21	75.0	1950	7	ADB78607	Adb78607 Human sod
66	21	75.0	1951	4	AAB99678	Aab99678 Human adu
67	21	75.0	1951	4	AAB99679	Aab99679 Human neo
68	21	75.0	1951	7	ADE59628	Ade59628 Rat Prote
69	21	75.0	1951	8	ADL06576	Adl06576 Human tum
70	21	75.0	2000	5	ABB06027	Abb06027 Human sod
71	21	75.0	2000	8	ADK81762	Adk81762 Human Nav
72	21	75.0	2015	4	AAB82242	Aab82242 Human SCN
73	21	75.0	2015	7	ADF56441	Adf56441 Human Nav
74	21	75.0	2015	8	ADM34001	Adm34001 Human SCN
75	21	75.0	2015	8	ADM33999	Adm33999 Human SCN
76	21	75.0	2016	2	AAW23994	Aaw23994 Human hH1
77	21	75.0	2016	4	AAB82239	Aab82239 Human SCN
78	21	75.0	2016	4	AAB82240	Aab82240 Human SCN
79	21	75.0	2016	4	AAB82245	Aab82245 Human SCN
80	21	75.0	2016	4	AAB82243	Aab82243 Human SCN
81	21	75.0	2016	4	AAB82244	Aab82244 Human SCN
82	21	75.0	2016	4	AAB82241	Aab82241 Human SCN
83	21	75.0	2016	7	ADD44756	Add44756 Human Pro
84	21	75.0	2016	7	ADE55106	Ade55106 Human Pro
85	21	75.0	2016	8	ADM33997	Adm33997 Human SCN
86	21	75.0	2016	8	ADM33995	Adm33995 Human SCN
87	21	75.0	2019	2	AAR67913	Aar67913 Cardiac s
88	17	60.7	2100	2	AAW89579	Aaw89579 Calcium p
89	17	60.7	2105	2	AAW57772	Aaw57772 Musca dom
90	17	60.7	2105	2	AAW89577	Aaw89577 Calcium p
91	17	60.7	2131	4	ABB64743	Abb64743 Drosophil
92	17	60.7	2131	8	ADI30141	Adi30141 Drosophil
93	17	60.7	2131	8	ADI30146	Adi30146 Drosophil
94	16	57.1	1011	2	AAR99638	Aar99638 Periphera
95	16	57.1	2009	7	ADE57561	Ade57561 Rat Prote
96	13	46.4	115	5	ABG37774	Abg37774 Human pep
97	12	42.9	2104	2	AAW57773	Aaw57773 Musca dom
98	12	42.9	2104	2	AAW89578	Aaw89578 Calcium p

99	10	35.7	125	8	ABO54760	Abo54760 Human gen
100	10	35.7	2020	2	AAR06584	Aar06584 Cardiac s

ALIGNMENTS

RESULT 1
ADB78596
ID ADB78596 standard; protein; 1795 AA.
XX
AC ADB78596;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:140.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78635.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 140; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 1795 AA;

Query Match 100.0%; Score 28; DB 7; Length 1795;
Best Local Similarity 100.0%; Pred. No. 6.7e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995

RESULT 2
ADB78597
ID ADB78597 standard; protein; 1855 AA.
XX
AC ADB78597;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:141.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78636.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 141; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human

CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 1855 AA;

Query Match 100.0%; Score 28; DB 7; Length 1855;
Best Local Similarity 100.0%; Pred. No. 6.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995

RESULT 3
ABR83185
ID ABR83185 standard; protein; 1981 AA.
XX
AC ABR83185;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human SCN1A splice variant -84P:SCN1ADELp654-681.
XX
KW SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
KW neuroprotective; anesthetic; cytostatic; cerebroprotective; cardiant;
KW hypotensive; gene therapy; human; splice variant.
XX
OS Homo sapiens.
XX
PN WO2003072751-A2.
XX
PD 04-SEP-2003.
XX
PF 25-FEB-2003; 2003WO-US006010.
XX
PR 25-FEB-2002; 2002US-0359382P.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI George AL, Lossin C;
XX
DR WPI; 2003-712725/67.
DR N-PSDB; ACF57880.
XX
PT Recombinantly expressed sodium channel type 1 alpha subunit, useful in
PT screening for modulators, for treating e.g. epilepsy.
XX
PS Disclosure; Page 162-169; 176pp; English.
XX
CC The invention relates to a recombinantly expressed and isolated human
CC SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
CC incorporated into a cell, is used to screen for specific modulators,
CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,
CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
CC motor endplate diseases, hypertension, congestive heart failure and
CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
CC and metastatic cancer cell lines). These activities can also be provided
CC by gene therapy vectors that express (I) or the modulators. The
CC modulators, also antibodies directed against (I), are used to detect
CC sodium channel polypeptides. The present sequence represents a human
CC SCN1A splice variant 84P:SCN1ADELp654-681
XX
SQ Sequence 1981 AA;

Query Match 100.0%; Score 28; DB 7; Length 1981;
Best Local Similarity 100.0%; Pred. No. 7.3e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 940 CLTVFMMVMVIGNLVVLNLFLALLLSSF 967

RESULT 4
ABR83184
ID ABR83184 standard; protein; 1998 AA.
XX
AC ABR83184;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human SCN1A splice variant -33P:SCN1ADELp671-681.
XX
KW SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
KW neuroprotective; anesthetic; cytostatic; cerebroprotective; cardiant;
KW hypotensive; gene therapy; human; splice variant.
XX
OS Homo sapiens.
XX
PN WO2003072751-A2.
XX
PD 04-SEP-2003.
XX
PF 25-FEB-2003; 2003WO-US006010.
XX
PR 25-FEB-2002; 2002US-0359382P.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI George AL, Lossin C;
XX
DR WPI; 2003-712725/67.
DR N-PSDB; ACF57879.
XX
PT Recombinantly expressed sodium channel type 1 alpha subunit, useful in
PT screening for modulators, for treating e.g. epilepsy.
XX
PS Disclosure; Page 148-156; 176pp; English.
XX
CC The invention relates to a recombinantly expressed and isolated human
CC SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
CC incorporated into a cell, is used to screen for specific modulators,
CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,
CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
CC motor endplate diseases, hypertension, congestive heart failure and
CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
CC and metastatic cancer cell lines). These activities can also be provided
CC by gene therapy vectors that express (I) or the modulators. The
CC modulators, also antibodies directed against (I), are used to detect
CC sodium channel polypeptides. The present sequence represents a human
CC SCN1A splice variant 33P:SCN1ADELp671-681 encoding cDNA
XX
SQ Sequence 1998 AA;

Query Match 100.0%; Score 28; DB 7; Length 1998;
Best Local Similarity 100.0%; Pred. No. 7.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 957 CLTVFMMVMVIGNLVVLNLFLALLLSSF 984

RESULT 5
ABB06026
ID ABB06026 standard; protein; 1999 AA.
XX
AC ABB06026;
XX
DT 10-MAY-2002 (first entry)
XX
DE Human sodium channel SCN1A protein SEQ ID NO:2.
XX
KW Human; sodium channel; SCN1A; chromosome 2q24;
KW familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
OS Homo sapiens.
XX
PN WO200196552-A1.
XX
PD 20-DEC-2001.
XX
PF 12-JUN-2001; 2001WO-JP004956.
XX
PR 13-JUN-2000; 2000JP-00177540.
PR 13-JUN-2000; 2000JP-00177544.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Kanazawa I, Goto J, Jeong S;
XX
DR WPI; 2002-098066/13.
DR N-PSDB; ABL39689.
XX
PT Human sodium channels SCN1A and SCN3A and encoded genes, useful in
PT studying physiological mechanism in which excitant cells participate and
PT causes of diseases and developing drugs for motor endplate disease.
XX
PS Claim 1; Page 40-49; 88pp; Japanese.
XX
CC The present invention describes human sodium channels SCN1A and SCN3A.
CC The present sequence represents the human sodium channel SCN1A. SCN1A and
CC SCN3A have been located to the human chromosome 2 long arm, positions
CC 2q24 and 2q24-31 respectively. The sodium channel proteins are useful in
CC studying the physiological mechanism in which excitant cells participate
CC and cause human diseases, and in developing remedies for e.g. familial
CC hypercalcaemic periodic paralysis of extremities and motor endplate
CC disease
XX
SQ Sequence 1999 AA;

Query Match 100.0%; Score 28; DB 5; Length 1999;
Best Local Similarity 100.0%; Pred. No. 7.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 958 CLTVFMMVMVIGNLVVLNLFLALLLSSF 985

RESULT 6
AAB99676
ID AAB99676 standard; protein; 2005 AA.
XX
AC AAB99676;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human adult form of SCN2A protein sequence SEQ ID NO:35.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA001404.
XX
PR 26-NOV-1999; 99US-0167623P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR N-PSDB; AAH55793.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
PS Disclosure; Page 123-130; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 4; Length 2005;
Best Local Similarity 100.0%; Pred. No. 7.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 959 CLTVFMMVMVIGNLVVLNLFLALLLSSF 986

RESULT 7
AAB99677
ID AAB99677 standard; protein; 2005 AA.
XX
AC AAB99677;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human neonatal form of SCN2A protein sequence SEQ ID NO:36.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA001404.
XX
PR 26-NOV-1999; 99US-0167623P.
XX

PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR N-PSDB; AAH55794.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
PS Disclosure; Page 131-138; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 4; Length 2005;
Best Local Similarity 100.0%; Pred. No. 7.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 959 CLTVFMMVMVIGNLVVLNLFLALLLSSF 986

RESULT 8
ABB83627
ID ABB83627 standard; protein; 2005 AA.
XX
AC ABB83627;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human GEFS+ protein with SCN2A mutation.
XX
KW Human; GEFS+; SCN2A; mutant; mutein;
KW generalized epilepsy with febrile seizure plus.
XX
OS Homo sapiens.
XX
PN JP2002136289-A.
XX
PD 14-MAY-2002.
XX
PF 01-NOV-2000; 2000JP-00334969.
XX
PR 01-NOV-2000; 2000JP-00334969.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (RIKA) RIKAGAKU KENKYUSHO.
XX
DR WPI; 2002-552308/59.
DR N-PSDB; ABQ79201.
XX
PT A human polynucleotide which is complementary to an mRNA transcribed from
PT a generalized epilepsy with febrile seizure plus (GEFS+)-related gene
PT useful for diagnosing GEFS+.
XX
PS Claim 10; Page 29-34; 37pp; Japanese.
XX
CC This invention relates to a human polynucleotide which is complementary
CC to an mRNA transcribed from a "generalized epilepsy with febrile seizure
CC plus" (GEFS+)-related gene. The gene is useful for diagnosing GEFS+. The
CC present sequence represents the human GEFS+ protein sequence with SCN2A
CC mutation
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 5; Length 2005;
Best Local Similarity 100.0%; Pred. No. 7.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 959 CLTVFMMVMVIGNLVVLNLFLALLLSSF 986

RESULT 9
ADB78604
ID ADB78604 standard; protein; 2005 AA.
XX
AC ADB78604;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:148.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78643.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 148; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an

CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 7; Length 2005;
Best Local Similarity 100.0%; Pred. No. 7.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 959 CLTVFMMVMVIGNLVVLNLFLALLLSSF 986

RESULT 10
ADB78603
ID ADB78603 standard; protein; 2005 AA.
XX
AC ADB78603;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:147.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78642.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 147; 106pp; English.
XX

CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 7; Length 2005;
Best Local Similarity 100.0%; Pred. No. 7.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 959 CLTVFMMVMVIGNLVVLNLFLALLLSSF 986

RESULT 11
ADB78605
ID ADB78605 standard; protein; 2005 AA.
XX
AC ADB78605;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:149.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.

DR N-PSDB; ADB78644.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 149; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 7; Length 2005;
Best Local Similarity 100.0%; Pred. No. 7.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 959 CLTVFMMVMVIGNLVVLNLFLALLLSSF 986

RESULT 12
ADC46947
ID ADC46947 standard; protein; 2005 AA.
XX
AC ADC46947;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human SCN2A amino acid sequence #SEQ ID 3.
XX
KW SCN2A; voltage-gated ion channel; human; neuroprotective; gene therapy;
KW vaccine; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO2003060525-A1.
XX
PD 24-JUL-2003.
XX
PF 16-JAN-2003; 2003WO-EP000400.
XX
PR 17-JAN-2002; 2002EP-00001236.
PR 17-JAN-2002; 2002US-0348674P.
XX
PA (EVOT-) EVOTEC NEUROSCIENCES GMBH.
XX
PI Hipfel R, Von Der Kammer H, Pohlner J;
XX
DR WPI; 2003-598580/56.
DR N-PSDB; ADC46961.
XX
PT Diagnosing or prognosticating a neurodegenerative disease by detecting
PT the level or activity of transcription or translation products of the
PT gene coding for the voltage-gated ion channel SCN2A.
XX
PS Disclosure; Fig 9; 67pp; English.
XX
CC The invention relates to a method for diagnosing or prognosticating a
CC neurodegenerative disease in a subject, or determining whether a subject
CC is at increased risk of developing the disease. The method comprises
CC detecting the level and/or activity of a transcription or translation
CC product of the gene coding for the voltage-gated ion channel SCN2A. The
CC modulator of an activity and/or of a level of at least one substance is
CC useful for preparing a composition for treating or preventing a
CC neurodegenerative disease, in particular Alzheimer's disease. The current
CC sequence represents the human SCN2A amino acid sequence.
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 7; Length 2005;
Best Local Similarity 100.0%; Pred. No. 7.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 959 CLTVFMMVMVIGNLVVLNLFLALLLSSF 986

RESULT 13
AAB99674
ID AAB99674 standard; protein; 2009 AA.
XX
AC AAB99674;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human adult form of SCN1A protein sequence SEQ ID NO:3.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA001404.
XX
PR 26-NOV-1999; 99US-0167623P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR N-PSDB; AAH55763.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
PS Disclosure; Page 96-104; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which

CC shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
XX
SQ Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 4; Length 2009;
Best Local Similarity 100.0%; Pred. No. 7.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995

RESULT 14
ABG69292
ID ABG69292 standard; protein; 2009 AA.
XX
AC ABG69292;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human sodium channel alpha 1-subunit (SCNA1) variant protein #4.
XX
KW Human; sodium channel alpha 1-subunit; SCN1A; episodic ataxia; epilepsy;
KW generalised epilepsy with febrile seizures plus; myasthenia;
KW sodium channel dysfunction; malignant hyperthermia; neuropathic pain;
KW inflammatory pain; Alzheimer's disease; Parkinson's disease; myotonia;
KW schizophrenia; hyperekplexia; anticonvulsant; analgesic; neuroprotective;
KW nootropic; anti-Parkinsonian; neuroleptic.
XX
OS Homo sapiens.
XX
PN WO200250096-A1.
XX
PD 27-JUN-2002.
XX
PF 20-DEC-2001; 2001WO-AU001648.
XX
PR 20-DEC-2000; 2000AU-00002203.
XX
PA (BION-) BIONOMICS LTD.
XX
PI Wallace RH, Mulley JC, Berkovic SF;
XX
DR WPI; 2002-528445/56.
XX
PT New nucleic acid encoding mutant alpha subunit of a mammalian voltage-
PT gated sodium channel, useful for diagnosis of epilepsy, particularly
PT generalized epilepsy with febrile seizures plus.
XX
PS Claim 53; Page 147-157; 198pp; English.
XX
CC The invention relates to a nucleic acid molecule encoding a mutant alpha
CC subunit of a mammalian voltage-gated sodium channel. The DNA and the
CC polypeptide may be used in the diagnosis of epilepsy, in particular
CC generalised epilepsy with febrile seizures plus, and other disorders
CC associated with sodium channel dysfunction. The polypeptide is useful for
CC the screening of candidate pharmaceutical agents, where high throughput
CC screening techniques are employed. The sequences are also useful in the
CC manufacture of a medicament for the treatment of a disorder associated
CC with sodium channel dysfunction such as epilepsy, particularly
CC generalised epilepsy with febrile seizures plus, malignant hyperthermia,
CC myasthenia, episodic ataxia, neuropathic and inflammatory pain,
CC Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia
CC and myotonias. Sequences ABG69289-ABG69293 represent human sodium channel
CC alpha 1-subunit (SCN1A) polypeptides of the invention
XX
SQ Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 5; Length 2009;
Best Local Similarity 100.0%; Pred. No. 7.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995

RESULT 15
ABG69291
ID ABG69291 standard; protein; 2009 AA.
XX
AC ABG69291;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human sodium channel alpha 1-subunit (SCNA1) variant protein #3.
XX
KW Human; sodium channel alpha 1-subunit; SCN1A; episodic ataxia; epilepsy;
KW generalised epilepsy with febrile seizures plus; myasthenia;
KW sodium channel dysfunction; malignant hyperthermia; neuropathic pain;
KW inflammatory pain; Alzheimer's disease; Parkinson's disease; myotonia;
KW schizophrenia; hyperekplexia; anticonvulsant; analgesic; neuroprotective;
KW nootropic; anti-Parkinsonian; neuroleptic.
XX
OS Homo sapiens.
XX
PN WO200250096-A1.
XX
PD 27-JUN-2002.
XX
PF 20-DEC-2001; 2001WO-AU001648.
XX
PR 20-DEC-2000; 2000AU-00002203.
XX
PA (BION-) BIONOMICS LTD.
XX
PI Wallace RH, Mulley JC, Berkovic SF;
XX
DR WPI; 2002-528445/56.
DR N-PSDB; ABK98843.
XX
PT New nucleic acid encoding mutant alpha subunit of a mammalian voltage-
PT gated sodium channel, useful for diagnosis of epilepsy, particularly
PT generalized epilepsy with febrile seizures plus.
XX
PS Claim 47; Page 107-117; 198pp; English.
XX
CC The invention relates to a nucleic acid molecule encoding a mutant alpha
CC subunit of a mammalian voltage-gated sodium channel. The DNA and the
CC polypeptide may be used in the diagnosis of epilepsy, in particular
CC generalised epilepsy with febrile seizures plus, and other disorders
CC associated with sodium channel dysfunction. The polypeptide is useful for
CC the screening of candidate pharmaceutical agents, where high throughput
CC screening techniques are employed. The sequences are also useful in the
CC manufacture of a medicament for the treatment of a disorder associated
CC with sodium channel dysfunction such as epilepsy, particularly
CC generalised epilepsy with febrile seizures plus, malignant hyperthermia,
CC myasthenia, episodic ataxia, neuropathic and inflammatory pain,
CC Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia
CC and myotonias. Sequences ABG69289-ABG69293 represent human sodium channel
CC alpha 1-subunit (SCN1A) polypeptides of the invention
XX
SQ Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 5; Length 2009;
Best Local Similarity 100.0%; Pred. No. 7.5e-18;

```
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||||||||
Db        968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995


RESULT 16
ABG69293
ID   ABG69293 standard; protein; 2009 AA.
XX
AC   ABG69293;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human sodium channel alpha 1-subunit (SCNA1) variant protein #5.
XX
KW   Human; sodium channel alpha 1-subunit; SCN1A; episodic ataxia; epilepsy;
KW   generalised epilepsy with febrile seizures plus; myasthenia;
KW   sodium channel dysfunction; malignant hyperthermia; neuropathic pain;
KW   inflammatory pain; Alzheimer's disease; Parkinson's disease; myotonia;
KW   schizophrenia; hyperekplexia; anticonvulsant; analgesic; neuroprotective;
KW   nootropic; anti-Parkinsonian; neuroleptic.
XX
OS   Homo sapiens.
XX
PN   WO200250096-A1.
XX
PD   27-JUN-2002.
XX
PF   20-DEC-2001; 2001WO-AU001648.
XX
PR   20-DEC-2000; 2000AU-00002203.
XX
PA   (BION-) BIONOMICS LTD.
XX
PI   Wallace RH,  Mulley JC,  Berkovic SF;
XX
DR   WPI; 2002-528445/56.
XX
PT   New nucleic acid encoding mutant alpha subunit of a mammalian voltage-
PT   gated sodium channel, useful for diagnosis of epilepsy, particularly
PT   generalized epilepsy with febrile seizures plus.
XX
PS   Claim 53; Page 167-176; 198pp; English.
XX
CC   The invention relates to a nucleic acid molecule encoding a mutant alpha
CC   subunit of a mammalian voltage-gated sodium channel. The DNA and the
CC   polypeptide may be used in the diagnosis of epilepsy, in particular
CC   generalised epilepsy with febrile seizures plus, and other disorders
CC   associated with sodium channel dysfunction. The polypeptide is useful for
CC   the screening of candidate pharmaceutical agents, where high throughput
CC   screening techniques are employed. The sequences are also useful in the
CC   manufacture of a medicament for the treatment of a disorder associated
CC   with sodium channel dysfunction such as epilepsy, particularly
CC   generalised epilepsy with febrile seizures plus, malignant hyperthermia,
CC   myasthenia, episodic ataxia, neuropathic and inflammatory pain,
CC   Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia
CC   and myotonias. Sequences ABG69289-ABG69293 represent human sodium channel
CC   alpha 1-subunit (SCN1A) polypeptides of the invention
XX
SQ   Sequence 2009 AA;

  Query Match             100.0%;  Score 28;  DB 5;  Length 2009;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||||||||
Db        968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995


RESULT 17
ABG69289
ID   ABG69289 standard; protein; 2009 AA.
XX
AC   ABG69289;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human sodium channel alpha 1-subunit (SCNA1) variant protein #1.
XX
KW   Human; sodium channel alpha 1-subunit; SCN1A; episodic ataxia; epilepsy;
KW   generalised epilepsy with febrile seizures plus; myasthenia;
KW   sodium channel dysfunction; malignant hyperthermia; neuropathic pain;
KW   inflammatory pain; Alzheimer's disease; Parkinson's disease; myotonia;
KW   schizophrenia; hyperekplexia; anticonvulsant; analgesic; neuroprotective;
KW   nootropic; anti-Parkinsonian; neuroleptic.
XX
OS   Homo sapiens.
XX
PN   WO200250096-A1.
XX
PD   27-JUN-2002.
XX
PF   20-DEC-2001; 2001WO-AU001648.
XX
PR   20-DEC-2000; 2000AU-00002203.
XX
PA   (BION-) BIONOMICS LTD.
XX
PI   Wallace RH,  Mulley JC,  Berkovic SF;
XX
DR   WPI; 2002-528445/56.
DR   N-PSDB; ABK98841.
XX
PT   New nucleic acid encoding mutant alpha subunit of a mammalian voltage-
PT   gated sodium channel, useful for diagnosis of epilepsy, particularly
PT   generalized epilepsy with febrile seizures plus.
XX
PS   Claim 36; Page 68-77; 198pp; English.
XX
CC   The invention relates to a nucleic acid molecule encoding a mutant alpha
CC   subunit of a mammalian voltage-gated sodium channel. The DNA and the
CC   polypeptide may be used in the diagnosis of epilepsy, in particular
CC   generalised epilepsy with febrile seizures plus, and other disorders
CC   associated with sodium channel dysfunction. The polypeptide is useful for
CC   the screening of candidate pharmaceutical agents, where high throughput
CC   screening techniques are employed. The sequences are also useful in the
CC   manufacture of a medicament for the treatment of a disorder associated
CC   with sodium channel dysfunction such as epilepsy, particularly
CC   generalised epilepsy with febrile seizures plus, malignant hyperthermia,
CC   myasthenia, episodic ataxia, neuropathic and inflammatory pain,
CC   Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia
CC   and myotonias. Sequences ABG69289-ABG69293 represent human sodium channel
CC   alpha 1-subunit (SCN1A) polypeptides of the invention
XX
SQ   Sequence 2009 AA;

  Query Match             100.0%;  Score 28;  DB 5;  Length 2009;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||||||||
Db        968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995


RESULT 18
ABG69290
ID   ABG69290 standard; protein; 2009 AA.
XX
AC   ABG69290;
XX
DT   21-OCT-2002  (first entry)
XX
```

DE Human sodium channel alpha 1-subunit (SCNA1) variant protein #2.
XX
KW Human; sodium channel alpha 1-subunit; SCN1A; episodic ataxia; epilepsy;
KW generalised epilepsy with febrile seizures plus; myasthenia;
KW sodium channel dysfunction; malignant hyperthermia; neuropathic pain;
KW inflammatory pain; Alzheimer's disease; Parkinson's disease; myotonia;
KW schizophrenia; hyperekplexia; anticonvulsant; analgesic; neuroprotective;
KW nootropic; anti-Parkinsonian; neuroleptic.
XX
OS Homo sapiens.
XX
PN WO200250096-A1.
XX
PD 27-JUN-2002.
XX
PF 20-DEC-2001; 2001WO-AU001648.
XX
PR 20-DEC-2000; 2000AU-00002203.
XX
PA (BION-) BIONOMICS LTD.
XX
PI Wallace RH, Mulley JC, Berkovic SF;
XX
DR WPI; 2002-528445/56.
DR N-PSDB; ABK98842.
XX
PT New nucleic acid encoding mutant alpha subunit of a mammalian voltage-
PT gated sodium channel, useful for diagnosis of epilepsy, particularly
PT generalized epilepsy with febrile seizures plus.
XX
PS Claim 42; Page 88-97; 198pp; English.
XX
CC The invention relates to a nucleic acid molecule encoding a mutant alpha
CC subunit of a mammalian voltage-gated sodium channel. The DNA and the
CC polypeptide may be used in the diagnosis of epilepsy, in particular
CC generalised epilepsy with febrile seizures plus, and other disorders
CC associated with sodium channel dysfunction. The polypeptide is useful for
CC the screening of candidate pharmaceutical agents, where high throughput
CC screening techniques are employed. The sequences are also useful in the
CC manufacture of a medicament for the treatment of a disorder associated
CC with sodium channel dysfunction such as epilepsy, particularly
CC generalised epilepsy with febrile seizures plus, malignant hyperthermia,
CC myasthenia, episodic ataxia, neuropathic and inflammatory pain,
CC Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia
CC and myotonias. Sequences ABG69289-ABG69293 represent human sodium channel
CC alpha 1-subunit (SCN1A) polypeptides of the invention
XX
SQ Sequence 2009 AA;

```
  Query Match             100.0%;  Score 28;  DB 5;  Length 2009;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||||||||
Db        968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995
```

RESULT 19
ABB83626
ID ABB83626 standard; protein; 2009 AA.
XX
AC ABB83626;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human GEFS+ protein with SCN1A mutation.
XX
KW Human; GEFS+; SCN1A; mutant; mutein;
KW generalized epilepsy with febrile seizure plus.
XX
OS Homo sapiens.
XX
PN JP2002136289-A.
XX
PD 14-MAY-2002.
XX
PF 01-NOV-2000; 2000JP-00334969.
XX
PR 01-NOV-2000; 2000JP-00334969.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (RIKA) RIKAGAKU KENKYUSHO.
XX
DR WPI; 2002-552308/59.
DR N-PSDB; ABQ79200.
XX
PT A human polynucleotide which is complementary to an mRNA transcribed from
PT a generalized epilepsy with febrile seizure plus (GEFS+)-related gene
PT useful for diagnosing GEFS+.
XX
PS Claim 11; Page 16-21; 37pp; Japanese.
XX
CC This invention relates to a human polynucleotide which is complementary
CC to an mRNA transcribed from a "generalized epilepsy with febrile seizure
CC plus" (GEFS+)-related gene. The gene is useful for diagnosing GEFS+. The
CC present sequence represents the human GEFS+ protein sequence with SCN1A
CC mutation
XX
SQ Sequence 2009 AA;

```
  Query Match             100.0%;  Score 28;  DB 5;  Length 2009;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||||||||
Db        968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995
```

RESULT 20
AAE16776
ID AAE16776 standard; protein; 2009 AA.
XX
AC AAE16776;
XX
DT 09-APR-2002 (first entry)
XX
DE Human transporter and ion channel-13 (TRICH-13) protein.
XX
KW Human; transporter and ion channel-13; TRICH-13; neuroprotective; asthma;
KW nootropic; cytostatic; cardiovascular; immunosuppressive; cardiomyopathy;
KW antiinflammatory; protein therapy; akinesia; cystic fibrosis; leukaemia;
KW Bell's palsy; amyotrophic lateral sclerosis; Alzheimer's disease; cancer;
KW amnesia; dementia; myocarditis; Duchenne's muscular dystrophy; AIDS;
KW Acquired Immune Deficiency Syndrome; Addison's disease; allergy; angina;
KW cell proliferative disorder; psoriasis; cardiac disease; hypertension;
KW bradyarrythmia; gene expression; drug screening.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Domain	122. .147
FT		/label= Transmembrane_domain
FT	Domain	124. .422
FT		/note= "Ion transport protein domain"
FT	Domain	213. .230
FT		/label= Transmembrane_domain
FT	Domain	250. .268
FT		/label= Transmembrane_domain
FT	Domain	399. .422
FT		/label= Transmembrane_domain
FT	Domain	761. .781
FT		/label= Transmembrane_domain
FT	Domain	764. .991
FT		/note= "Ion transport protein domain"

```
FT   Domain          803. .821
FT                   /label= Transmembrane_domain
FT   Domain          832. .852
FT                   /label= Transmembrane_domain
FT   Domain          893. .911
FT                   /label= Transmembrane_domain
FT   Binding-site    908. .915
FT                   /label= P_loop
FT                   /note= "ATP/GTP binding site"
FT   Domain          971. .991
FT                   /label= Transmembrane_domain
FT   Domain          1214. .1482
FT                   /note= "Ion transport protein domain"
FT   Domain          1251. .1274
FT                   /label= Transmembrane_domain
FT   Domain          1350. .1369
FT                   /label= Transmembrane_domain
FT   Domain          1459. .1482
FT                   /label= Transmembrane_domain
FT   Domain          1537. .1785
FT                   /note= "Ion transport protein domain"
FT   Domain          1543. .1562
FT                   /label= Transmembrane_domain
FT   Domain          1576. .1594
FT                   /label= Transmembrane_domain
FT   Domain          1602. .1620
FT                   /label= Transmembrane_domain
FT   Domain          1633. .1650
FT                   /label= Transmembrane_domain
FT   Domain          1673. .1692
FT                   /label= Transmembrane_domain
FT   Domain          1762. .1785
FT                   /label= Transmembrane_domain
FT   Binding-site    1916. .1936
FT                   /note= "IQ calmodulin-binding motif"
XX
PN   WO200192304-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US017065.
XX
PR   26-MAY-2000; 2000US-0208424P.
PR   01-JUN-2000; 2000US-0209001P.
PR   08-JUN-2000; 2000US-0210588P.
PR   16-JUN-2000; 2000US-0212335P.
PR   22-JUN-2000; 2000US-0213747P.
PR   29-JUN-2000; 2000US-0215391P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Thornton M,  Walia NK,  Yue H,  Nguyen DB,  Lai P,  Gandhi AR;
PI   Tribouley CM,  Yao MG,  Ramkumar J,  Au-Young J,  Lu Y,  Tang YT;
PI   Azimzai Y,  Bruns CM,  Griffin JA,  Yang J,  Sanjanwala MS,  Raumann BE;
PI   Lee EA,  Hafalia A,  Baughn MR,  Green BD,  Khan FA,  Kearney L;
PI   Elliot VS,  Seilhamer JJ,  Policky JL,  Borowsky ML,  Burford N,  Ding L;
PI   Lu DAM,  Hillman JL;
XX
DR   WPI; 2002-122055/16.
DR   N-PSDB; AAD27266.
XX
PT   New human transporters and ion channels (TRICH) polypeptides useful for
PT   diagnosing, treating or preventing disorders associated with aberrant
PT   expression of TRICH.
XX
PS   Claim 1; Page 158-162; 210pp; English.
XX
CC   The invention relates to human transporters and ion channels (TRICH)
CC   polypeptides and their cDNA molecules. The nucleic acid and polypeptide
CC   sequences are useful in the diagnosis, treatment, and prevention of
CC   disorders associated with transport (akinesia, cystic fibrosis, Bell's
CC   palsy, amyotrophic lateral sclerosis); neurological (Alzheimer's disease,
CC   amnesia, dementia); muscle (cardiomyopathy, myocarditis, Duchenne's
CC   muscular dystrophy); immunological (AIDS, Addison's disease, allergies,
CC   asthma); cell proliferative disorders (cancers, leukaemia, psoriasis);
CC   cardiac disease (angina, hypertension, or bradyarrythmia) and in the
CC   assessment of the effects of exogenous compounds on the expression of
CC   nucleic acid and amino acid sequences of transporters and ion channels.
CC   The polynucleotides may be used to detect and quantify gene expression in
CC   biopsied tissues in which TRICH expression may be correlated with a
CC   disease, to generate hybridization probes for mapping naturally occurring
CC   genomic sequence, and in drug screening. The present sequence is human
CC   TRICH-13 protein
XX
SQ   Sequence 2009 AA;

  Query Match             100.0%;  Score 28;  DB 5;  Length 2009;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||||||||
Db        968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995


RESULT 21
ADB78599
ID   ADB78599 standard; protein; 2009 AA.
XX
AC   ADB78599;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human sodium channel subunit mutant SEQ ID NO:143.
XX
KW   mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW   neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW   antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW   nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW   ion channel dysfunction; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003008574-A1.
XX
PD   30-JAN-2003.
XX
PF   08-JUL-2002; 2002WO-AU000910.
XX
PR   18-JUL-2001; 2001AU-00006452.
PR   05-MAR-2002; 2002AU-00000910.
PR   13-MAY-2002; 2002AU-00002292.
XX
PA   (BION-) BIONOMICS LTD.
PA   (WALL/) WALLACE R W.
XX
PI   Mulley JC,  Harkin LA,  Dibbens LM,  Phillips HA,  Heron SE;
PI   Berkovic SF,  Scheffer IE;
XX
DR   WPI; 2003-239332/23.
DR   N-PSDB; ADB78638.
XX
PT   Identifying predisposition to an ion channel dysfunction, such as
PT   periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT   schizophrenia, anxiety and depression, by detecting encoding-gene
PT   mutation events.
XX
PS   Claim 13; SEQ ID NO 143; 106pp; English.
XX
CC   The invention relates to a novel method for identifying a subject
CC   predisposed to a disorder associated with ion channel dysfunction. The
CC   method comprises ascertaining if at least one of the genes encoding ion
CC   channel subunits (ICS) has undergone a mutation event so that a cDNA
CC   derived from the subject has any of 134 nucleotide sequences. The method
CC   of the invention has nootropic, neuroprotective, inotropic, antipyretic,
```

CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 7; Length 2009;
Best Local Similarity 100.0%; Pred. No. 7.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995

RESULT 22
ADB78595
ID ADB78595 standard; protein; 2009 AA.
XX
AC ADB78595;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:139.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78634.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 139; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 7; Length 2009;
Best Local Similarity 100.0%; Pred. No. 7.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995

RESULT 23
ADB78593
ID ADB78593 standard; protein; 2009 AA.
XX
AC ADB78593;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:137.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;

PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78632.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 137; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 7; Length 2009;
Best Local Similarity 100.0%; Pred. No. 7.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995

RESULT 24
ADB78594
ID ADB78594 standard; protein; 2009 AA.
XX
AC ADB78594;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:138.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78633.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 138; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 7; Length 2009;
Best Local Similarity 100.0%; Pred. No. 7.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995

RESULT 25
ADB78598
ID ADB78598 standard; protein; 2009 AA.
XX
AC ADB78598;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:142.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.

XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78637.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 142; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 7; Length 2009;
Best Local Similarity 100.0%; Pred. No. 7.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995

Search completed: January 27, 2005, 17:45:15
Job time : 88.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:36:05 ; Search time 17 Seconds
(without alignments)
158.475 Million cell updates/sec

Title: US-10-608-584-13
Perfect score: 28
Sequence: 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	100.0	200	2	I48108	sodium channel alp
2	28	100.0	2005	2	A46269	sodium channel alp
3	28	100.0	2005	2	B25019	sodium channel pro
4	25	89.3	1976	2	I56555	sodium channel pro
5	23	82.1	1977	2	S54771	sodium channel alp
6	22	78.6	1835	2	I54323	sodium channel alp
7	22	78.6	1836	2	I64893	sodium channel alp
8	22	78.6	1836	2	JS0648	sodium channel alp
9	22	78.6	1836	2	I51964	sodium channel alp
10	22	78.6	1840	1	CHRTM1	sodium channel pro
11	21	75.0	1951	2	S00320	sodium channel pro
12	21	75.0	1983	2	A60054	sodium channel pro
13	21	75.0	2016	2	A38195	sodium channel pro
14	21	75.0	2019	2	A33996	sodium channel pro
15	18	64.3	1784	2	T43167	sodium channel pro
16	17	60.7	109	2	S72488	sodium channel pro
17	17	60.7	1034	2	S60051	sodium channel alp
18	17	60.7	1034	2	S60060	sodium channel alp
19	17	60.7	1689	2	S72467	sodium channel pro
20	17	60.7	1820	2	A33299	sodium channel pro
21	17	60.7	1993	2	T30902	sodium channel SCA
22	17	60.7	2049	2	T43161	sodium channel pro
23	17	60.7	2108	2	S72458	sodium channel pro
24	16	57.1	2009	2	A25019	sodium channel pro
25	14	50.0	1695	2	JE0084	voltage-gated sodi
26	12	42.9	1820	1	CHEE	sodium channel pro
27	11	39.3	1739	2	A48298	sodium channel hom
28	10	35.7	1321	2	A60165	sodium channel pro
29	10	35.7	1810	2	T31092	probable voltage-g
30	9	32.1	409	2	F89834	hypothetical prote
31	9	32.1	1957	2	S68453	sodium channel pro
32	8	28.6	501	2	I61512	TNF receptor assoc
33	8	28.6	616	2	AF0263	proteinase IV (EC
34	8	28.6	1699	2	T31340	voltage-gated sodi
35	7	25.0	33	2	A36154	benzphetamine N-de
36	7	25.0	68	2	S49412	fibrinogen-binding
37	7	25.0	100	2	S66718	probable membrane
38	7	25.0	101	2	S60632	NADH2 dehydrogenas
39	7	25.0	104	1	PFHU4A	platelet factor 4
40	7	25.0	116	2	B89887	hypothetical prote
41	7	25.0	118	2	S42598	hypothetical prote
42	7	25.0	155	2	S60647	NADH2 dehydrogenas
43	7	25.0	166	2	JC6559	interferon-gamma p
44	7	25.0	183	2	E72459	hypothetical prote
45	7	25.0	218	2	T19256	hypothetical prote
46	7	25.0	237	2	AF0772	probable exported
47	7	25.0	247	2	E86161	F10O3.11 protein -
48	7	25.0	257	2	H84597	hypothetical prote
49	7	25.0	292	2	A47125	transcription acti
50	7	25.0	358	2	T26231	hypothetical prote
51	7	25.0	386	2	AH3467	glycine betaine/l-
52	7	25.0	390	2	H70904	probable lprK prot
53	7	25.0	420	2	T39523	probable transmemb
54	7	25.0	451	2	H89798	conserved hypothet
55	7	25.0	480	2	G70302	conserved hypothet
56	7	25.0	505	2	AC1469	internalin like pr
57	7	25.0	513	2	A71004	hypothetical prote
58	7	25.0	538	2	G72539	probable CTP synth
59	7	25.0	578	2	AH1020	cytochrome c-type
60	7	25.0	721	2	F87611	TonB-dependent rec
61	7	25.0	1158	2	S57348	nuclear factor RIP
62	7	25.0	1172	2	T36053	probable ABC-type
63	7	25.0	1438	2	B71610	WD40 WEB-1 homolog
64	7	25.0	1582	2	A56248	sulfonylurea recep
65	7	25.0	1765	2	T42388	sodium channel alp
66	6	21.4	52	2	E96798	hypothetical prote
67	6	21.4	66	2	C97928	hypothetical prote
68	6	21.4	73	2	B83338	hypothetical prote
69	6	21.4	83	2	T03673	pit1 protein (clon
70	6	21.4	85	2	H83492	hypothetical prote
71	6	21.4	97	2	E95038	preprotein translo
72	6	21.4	97	2	H97908	conserved hypothet
73	6	21.4	100	1	F70309	protein export mem
74	6	21.4	102	2	C86365	probable 10kd chap
75	6	21.4	102	2	A75417	hypothetical prote
76	6	21.4	103	2	C71189	hypothetical prote
77	6	21.4	107	2	F71700	hypothetical prote
78	6	21.4	111	2	B70035	chaperonin homolog
79	6	21.4	117	2	AG3451	murein hydrolase e
80	6	21.4	120	2	S57057	probable membrane
81	6	21.4	123	2	A75273	hypothetical prote
82	6	21.4	123	2	T35812	probable small hyd
83	6	21.4	138	2	AD1850	hypothetical prote
84	6	21.4	139	2	E69744	hypothetical prote
85	6	21.4	149	2	F75327	hypothetical prote
86	6	21.4	158	2	G82494	conserved hypothet
87	6	21.4	164	2	S22204	photosystem I chai
88	6	21.4	165	2	B75502	hypothetical prote
89	6	21.4	166	1	IVBOG	interferon gamma p
90	6	21.4	166	2	S12723	interferon gamma p
91	6	21.4	166	2	S35795	androgen receptor
92	6	21.4	167	2	D75636	hypothetical prote
93	6	21.4	175	2	B95412	hypothetical prote
94	6	21.4	178	2	C72025	conserved hypothet
95	6	21.4	178	2	A86598	CT718 hypothetical
96	6	21.4	180	2	T15426	hypothetical prote
97	6	21.4	184	2	T38162	hypothetical RER1-
98	6	21.4	184	2	AB2503	hypothetical prote
99	6	21.4	185	2	T24345	hypothetical prote
100	6	21.4	185	2	S76706	hypothetical prote

ALIGNMENTS

RESULT 1
I48108
sodium channel alpha subunit - long-tailed hamster (fragment)
C;Species: Cricetulus longicaudatus (long-tailed hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48108
R;Lalik, P.H.; Krafte, D.S.; Ciccarelli, R.B.
Am. J. Physiol. 264, 803-809, 1993
A;Title: Characterization of endogenous Sodium channel gene expressed in chinese hamster
A;Reference number: I48107
A;Accession: I48108
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-200 <RES>
A;Cross-references: UNIPROT:Q60464; GB:M87541; NID:g191069; PIDN:AAA36979.1; PID:g553840
C;Genetics:
A;Gene: cho1
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 100.0%; Score 28; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 3.3e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 45 CLTVFMMVMVIGNLVVLNLFLALLLSSF 72

RESULT 2
A46269
sodium channel alpha chain HBA - human
C;Species: Homo sapiens (man)
C;Date: 20-Oct-1993 #sequence_revision 18-Nov-1994 #text_change 21-Nov-1997
C;Accession: A46269
R;Ahmed, C.M.; Ware, D.H.; Lee, S.C.; Patten, C.D.; Ferrer-Montiel, A.V.; Schinder, A.F.
Proc. Natl. Acad. Sci. U.S.A. 89, 8220-8224, 1992
A;Title: Primary structure, chromosomal localization, and functional expression of a vol
A;Reference number: A46269; MUID:92390418; PMID:1325650
A;Accession: A46269
A;Molecule type: mRNA
A;Residues: 1-2005 <AHM>
A;Cross-references: GB:M94055
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:113082)
C;Genetics:
A;Map position: 2q23-q24.3
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 100.0%; Score 28; DB 2; Length 2005;
Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 959 CLTVFMMVMVIGNLVVLNLFLALLLSSF 986

RESULT 3
B25019
sodium channel protein II - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: B25019; S24804
R;Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H
Nature 320, 188-192, 1986
A;Title: Existence of distinct sodium channel messenger RNAs in rat brain.
A;Reference number: A93377; MUID:86146901; PMID:3754035
A;Accession: B25019
A;Molecule type: mRNA
A;Residues: 1-2005 <NOD>
A;Cross-references: UNIPROT:Q63509
A;Experimental source: brain
R;Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
submitted to the EMBL Data Library, August 1991
A;Description: Developmentally regulated RNA splicing of rat brain sodium channel mRNAs.
A;Reference number: S24803
A;Accession: S24804
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 183-188,'D',190-305 <SAR>
A;Cross-references: EMBL:X61149; NID:g57074; PIDN:CAA43458.1; PID:g57076
C;Superfamily: sodium channel protein
C;Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-ga

Query Match 100.0%; Score 28; DB 2; Length 2005;
Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
||||||||||||||||||||||||||||
Db 959 CLTVFMMVMVIGNLVVLNLFLALLLSSF 986

RESULT 4
I56555
sodium channel protein 6 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56555
R;Schaller, K.L.; Krzemien, D.M.; Yarowsky, P.J.; Krueger, B.K.; Caldwell, J.H.
J. Neurosci. 15, 3231-3242, 1995
A;Title: A novel, abundant sodium channel expressed in neurons and glia.
A;Reference number: I56555; MUID:95271284; PMID:7751906
A;Accession: I56555
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1976 <RES>
A;Cross-references: UNIPROT:Q63541; GB:L39018; NID:g829033; PIDN:AAC42059.1; PID:g829034
C;Genetics:
A;Gene: SCP6
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 89.3%; Score 25; DB 2; Length 1976;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFMMVMVIGNLVVLNLFLALLLSSF 28
|||||||||||||||||||||||||
Db 952 VFMMVMVIGNLVVLNLFLALLLSSF 976

RESULT 5
S54771
sodium channel alpha subunit - human
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54771
R;Klugbauer, N.; Lacinova, L.; Flockerzi, V.; Hofmann, F.
EMBO J. 14, 1084-1090, 1995
A;Title: Structure and functional expression of a new member of the tetrodotoxin-sensiti
A;Reference number: S54771; MUID:95237189; PMID:7720699
A;Accession: S54771
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1977 <KLU>
A;Cross-references: UNIPROT:Q15858; EMBL:X82835; NID:g758109; PIDN:CAA58042.1; PID:g7581
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 82.1%; Score 23; DB 2; Length 1977;

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  Best Local Similarity   100.0%;  Pred. No. 1.2e-13;
  Matches    23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        938 MMVMVIGNLVVLNLFLALLLSSF 960


RESULT 6
I54323
sodium channel alpha subunit - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C;Accession: I54323
R;McClatchey, A.I.; Lin, C.S.; Wang, J.; Hoffman, E.P.; Rojas, C.; Gusella, J.F.
Hum. Mol. Genet. 1, 521-527, 1992
A;Title: The genomic structure of the human skeletal muscle sodium channel gene.
A;Reference number: I54323; MUID:93338444; PMID:1339144
A;Accession: I54323
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1835 <RES>
A;Cross-references: GB:L01983; NID:g337992; PIDN:AAA75557.1; PID:g908809
C;Genetics:
A;Gene: GDB:SCN4A
A;Cross-references: GDB:125181; OMIM:170500
A;Map position: 17q23.1-17q25.3
A;Introns: 91/3; 131/2; 161/2; 204/2; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/3; 6
C;Superfamily: sodium channel protein
C;Keywords: duplication

  Query Match             78.6%;  Score 22;  DB 2;  Length 1835;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-13;
  Matches    22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 MVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        784 MVMVIGNLVVLNLFLALLLSSF 805


RESULT 7
I64893
sodium channel alpha subunit - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: I64893
R;George, A.L.
Ann. Neurol. 31, 131-137, 1992
A;Title: Primary structure of the adult human skeletal muscle voltage-dependent sodium c
A;Reference number: I51964; MUID:92246457; PMID:1315496
A;Accession: I64893
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1836 <RES>
A;Cross-references: UNIPROT:P35499; GB:M81758; NID:g338212; PIDN:AAA60554.1; PID:g338213
C;Genetics:
A;Gene: SkM1
C;Superfamily: sodium channel protein
C;Keywords: duplication

  Query Match             78.6%;  Score 22;  DB 2;  Length 1836;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-13;
  Matches    22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 MVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        784 MVMVIGNLVVLNLFLALLLSSF 805


RESULT 8
JS0648
sodium channel alpha chain - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JS0648; A42099
R;Wang, J.; Rojas, C.V.; Zhou, J.; Schwartz, L.S.; Nicholas, H.; Hoffmann, E.P.
Biochem. Biophys. Res. Commun. 182, 794-801, 1992
A;Title: Sequence and genomic structure of the human adult skeletal muscle sodium channe
A;Reference number: JS0648; MUID:92134303; PMID:1310396
A;Accession: JS0648
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1836 <WAN>
A;Cross-references: UNIPROT:P35499
A;Note: 861-Asp was also found as the result of polymorphism
R;McClatchey, A.I.; Van den Bergh, P.; Pericak-Vance, M.A.; Raskind, W.; Verellen, C.; Mc
Cell 68, 769-774, 1992
A;Title: Temperature-sensitive mutations in the III-IV cytoplasmic loop region of the ske
A;Reference number: A42099; MUID:92154689; PMID:1310898
A;Accession: A42099
A;Molecule type: DNA
A;Residues: 1299-1351 <MCC>
A;Cross-references: GB:S82622; NID:g245611; PIDN:AAB21450.1; PID:g245612
A;Experimental source: skeletal muscle
A;Note: sequence extracted from NCBI backbone (NCBIN:82622, NCBIP:82623)
C;Genetics:
A;Gene: GDB:SCN4A
A;Cross-references: GDB:125181; OMIM:170500
A;Map position: 17q23.1-17q25.3
C;Superfamily: sodium channel protein
C;Keywords: duplication; glycoprotein; phosphoprotein; transmembrane protein
F;129-150/Domain: transmembrane #status predicted <TR1>
F;159-178/Domain: transmembrane #status predicted <TR2>
F;191-210/Domain: transmembrane #status predicted <TR3>
F;217-236/Domain: transmembrane #status predicted <TR4>
F;253-266/Domain: transmembrane #status predicted <TR5>
F;424-449/Domain: transmembrane #status predicted <TR6>
F;574-597/Domain: transmembrane #status predicted <RI1>
F;609-632/Domain: transmembrane #status predicted <RI2>
F;641-660/Domain: transmembrane #status predicted <RI3>
F;667-686/Domain: transmembrane #status predicted <RI4>
F;702-724/Domain: transmembrane #status predicted <RI5>
F;777-802/Domain: transmembrane #status predicted <RI6>
F;1027-1049/Domain: transmembrane #status predicted <II1>
F;1064-1089/Domain: transmembrane #status predicted <II2>
F;1096-1116/Domain: transmembrane #status predicted <II3>
F;1122-1143/Domain: transmembrane #status predicted <II4>
F;1163-1184/Domain: transmembrane #status predicted <II5>
F;1269-1295/Domain: transmembrane #status predicted <II6>
F;1349-1372/Domain: transmembrane #status predicted <VS1>
F;1384-1407/Domain: transmembrane #status predicted <VS2>
F;1414-1437/Domain: transmembrane #status predicted <VS3>
F;1447-1469/Domain: transmembrane #status predicted <VS4>
F;1485-1507/Domain: transmembrane #status predicted <VS5>
F;1574-1598/Domain: transmembrane #status predicted <VS6>
F;21,149,220,378,415,1019,1130,1242,1313,1721,1826/Binding site: phosphate (Thr) (covale
F;56,251,513,653,1511,1746/Binding site: phosphate (Ser) (covalent) (by protein kinase A
F;214,288,291,297,303,315,321,333,362,507,702,961,1191,1205/Binding site: carbohydrate (
F;246,670,725,850,950,1127,1195,1328/Binding site: phosphate (Ser) (covalent) (by protei
F;387,457/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predict

  Query Match             78.6%;  Score 22;  DB 2;  Length 1836;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-13;
  Matches    22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 MVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        784 MVMVIGNLVVLNLFLALLLSSF 805


RESULT 9
I51964
sodium channel alpha chain SCN4A, skeletal muscle - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I51964
```

```
R;George, A.L.
Ann. Neurol. 31, 131-137, 1992
A;Title: Primary structure of the adult human skeletal muscle voltage-dependent sodium c
A;Reference number: I51964; MUID:92246457; PMID:1315496
A;Accession: I51964
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1836 <RES>
A;Cross-references: UNIPROT:P35499; GB:L04236; NID:g292485; PIDN:AAB59624.1; PID:g292487
C;Genetics:
A;Gene: GDB:SCN4A
A;Cross-references: GDB:125181; OMIM:170500
A;Map position: 17q23.1-17q25.3
A;Introns: 91/3; 131/2; 161/2; 204/2; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/3; 6
C;Superfamily: sodium channel protein
C;Keywords: duplication; skeletal muscle

  Query Match             78.6%;  Score 22;  DB 2;  Length 1836;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-13;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 MVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||
Db        784 MVMVIGNLVVLNLFLALLLSSF 805


RESULT 10
CHRTM1
sodium channel protein mu1 alpha chain, skeletal muscle - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: JN0007
R;Trimmer, J.S.; Cooperman, S.S.; Tomiko, S.A.; Zhou, J.; Crean, S.M.; Boyle, M.B.; Kall
Neuron 3, 33-49, 1989
A;Title: Primary structure and functional expression of a mammalian skeletal muscle sodi
A;Reference number: JN0007; MUID:90148778; PMID:2559760
A;Accession: JN0007
A;Molecule type: mRNA
A;Residues: 1-1840 <TRI>
A;Cross-references: UNIPROT:P15390; GB:M26643; NID:g205651; PIDN:AAA41682.1; PID:g205652
C;Comment: Action potentials propagated by skeletal muscle sodium channels are responsib
C;Comment: This heavily glycosylated protein contains four homologous domains, each of w
C;Comment: This protein is distinct from but related to sodium channel proteins isolated
C;Superfamily: sodium channel protein
C;Keywords: duplication; glycoprotein; ion transport; neuromuscular junction; phosphopro
F;120-458,561-813,1013-1305,1335-1611/Region: duplication
F;56,251,1321,1504/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #
F;214,288,291,297,303,309,315,327,356,502,696,954,1184,1198,1563,1702/Binding site: carb

  Query Match             78.6%;  Score 22;  DB 1;  Length 1840;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-13;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 MVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||
Db        778 MVMVIGNLVVLNLFLALLLSSF 799


RESULT 11
S00320
sodium channel protein III - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S00320
R;Kayano, T.; Noda, M.; Flockerzi, V.; Takahashi, H.; Numa, S.
FEBS Lett. 228, 187-194, 1988
A;Title: Primary structure of rat brain sodium channel III deduced from the cDNA sequenc
A;Reference number: S00320; MUID:88137594; PMID:2449363
A;Accession: S00320
A;Molecule type: mRNA
A;Residues: 1-1951 <KAY>
A;Cross-references: UNIPROT:P08104; EMBL:Y00766; NID:g57210; PIDN:CAA68735.1; PID:g57211
A;Note: 270-Ile, 278-Leu, 355-Thr, 513-Lys, and 1059-Arg were also found
C;Superfamily: sodium channel protein
C;Keywords: duplication; transmembrane protein

  Query Match             75.0%;  Score 21;  DB 2;  Length 1951;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||
Db        918 VMVIGNLVVLNLFLALLLSSF 938


RESULT 12
A60054
sodium channel protein IIIb, long form - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60054; B44824
R;Joho, R.H.; Moorman, J.R.; VanDongen, A.M.J.; Kirsch, G.E.; Silberberg, H.; Schuster, (
Brain Res. Mol. Brain Res. 7, 105-113, 1990
A;Title: Toxin and kinetic profile of rat brain type III sodium channels expressed in Xe
A;Reference number: A60054; MUID:90251117; PMID:2160038
A;Accession: A60054
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1983 <JOH>
A;Cross-references: UNIPROT:Q64243
R;Schaller, K.L.; Krzemien, D.M.; McKenna, N.M.; Caldwell, J.H.
J. Neurosci. 12, 1370-1381, 1992
A;Title: Alternatively spliced sodium channel transcripts in brain and muscle.
A;Reference number: A44824; MUID:92211397; PMID:1313493
A;Accession: B44824
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 611-662 <SCH>
A;Cross-references: GB:S97388; NID:g248225; PIDN:AAB21984.1; PID:g248226
A;Experimental source: skeletal muscle
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:97388, NCBIP:97391)
C;Superfamily: sodium channel protein
C;Keywords: duplication; glycoprotein; ion transport; sodium channel; transmembrane prote

  Query Match             75.0%;  Score 21;  DB 2;  Length 1983;
  Best Local Similarity   100.0%;  Pred. No. 9e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||
Db        950 VMVIGNLVVLNLFLALLLSSF 970


RESULT 13
A38195
sodium channel protein hHI, cardiac - human
N;Alternate names: tetrodotoxin-insensitive, voltage-dependent sodium channel, TTX-I NaC
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A38195
R;Gellens, M.E.; George Jr., A.L.; Chen, L.Q.; Chahine, M.; Horn, R.; Barchi, R.L.; Kall
Proc. Natl. Acad. Sci. U.S.A. 89, 554-558, 1992
A;Title: Primary structure and functional expression of the human cardiac tetrodotoxin-i
A;Reference number: A38195; MUID:92115699; PMID:1309946
A;Accession: A38195
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-2016 <GEL>
A;Cross-references: UNIPROT:Q14524; GB:M77235; NID:g184038; PIDN:AAA58644.1; PID:g184039
A;Experimental source: heart
C;Superfamily: sodium channel protein
C;Keywords: cardiac muscle; duplication; glycoprotein; heart; ion transport; sodium chan

  Query Match             75.0%;  Score 21;  DB 2;  Length 2016;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-12;
```

```
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||
Db        922 VMVIGNLVVLNLFLALLLSSF 942


RESULT 14
A33996
sodium channel protein I, cardiac - rat
N;Alternate names: sodium channel protein (SkM2) alpha chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33996; JQ0412
R;Rogart, R.B.; Cribbs, L.L.; Muglia, L.K.; Kephart, D.D.; Kaiser, M.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 8170-8174, 1989
A;Title: Molecular cloning of a putative tetrodotoxin-resistant rat heart Na(+) channel
A;Reference number: A33996; MUID:90046760; PMID:2554302
A;Accession: A33996
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2019 <ROG>
A;Cross-references: UNIPROT:P15389; GB:M27902; NID:g206857; PIDN:AAA42114.1; PID:g206858
R;Kallen, R.G.; Sheng, Z.H.; Yang, J.; Chen, L.; Rogart, R.B.; Barchi, R.L.
Neuron 4, 233-242, 1990
A;Title: Primary structure and expression of a sodium channel characteristic of denervat
A;Reference number: JQ0412; MUID:90166613; PMID:2155010
A;Accession: JQ0412
A;Molecule type: mRNA
A;Residues: 1-479,481-1712,'T',1714-1963,'R',1965-2019 <KAL>
A;Experimental source: muscle
C;Superfamily: sodium channel protein
C;Keywords: cardiac muscle; duplication; heart; sodium channel; transmembrane protein

  Query Match             75.0%;  Score 21;  DB 2;  Length 2019;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||
Db        925 VMVIGNLVVLNLFLALLLSSF 945


RESULT 15
T43167
sodium channel protein - California market squid
C;Species: Loligo opalescens (California market squid)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43167
R;Rosenthal, J.J.; Gilly, W.F.
Proc. Natl. Acad. Sci. U.S.A. 90, 10026-10030, 1993
A;Title: Amino acid sequence of a putative sodium channel expressed in the giant axon of
A;Reference number: Z22324; MUID:94052096; PMID:8234251
A;Accession: T43167
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1784 <ROS>
A;Cross-references: UNIPROT:Q25377; EMBL:L19979; NID:g349118; PID:g349119; PIDN:AAA16202
A;Experimental source: stellate ganglia
C;Superfamily: sodium channel protein
C;Keywords: ion transport; membrane protein; sodium channel; voltage-gated ion channel

  Query Match             64.3%;  Score 18;  DB 2;  Length 1784;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-09;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 IGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||
Db        799 IGNLVVLNLFLALLLSSF 816


RESULT 16
S72488
sodium channel protein para-type alpha chain - house fly (strain SBO) (fragment)
C;Species: Musca domestica (house fly)
A;Variety: strain SBO
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
C;Accession: S72488
R;Miyazaki, M.; Ohyama, K.; Dunlap, D.Y.; Matsumura, F.
Mol. Gen. Genet. 252, 61-68, 1996
A;Title: Cloning and sequencing of the para-type sodium channel gene from susceptible an
A;Reference number: S72487; MUID:96397510; PMID:8804404
A;Accession: S72488
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-109 <MIY>
A;Cross-references: UNIPROT:Q25439; UNIPROT:Q25440; UNIPROT:Q94615; UNIPROT:Q95VP7
A;Experimental source: strain SBO
C;Superfamily: sodium channel protein
C;Keywords: sodium channel; transmembrane protein

  Query Match             60.7%;  Score 17;  DB 2;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-09;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 VIGNLVVLNLFLALLLS 26
              |||||||||||||||||
Db         71 VIGNLVVLNLFLALLLS 87


RESULT 17
S60051
sodium channel alpha chain, exon c-containing splice form - fruit fly (Drosophila virili
C;Species: Drosophila virilis
C;Date: 24-Aug-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C;Accession: S60051
R;Thackeray, J.R.; Ganetzky, B.
Genetics 141, 203-214, 1995
A;Title: Conserved alternative splicing patterns and splicing signals in the Drosophila
A;Reference number: S60051; MUID:96042905; PMID:8536968
A;Accession: S60051
A;Status: nucleic acid sequence not shown
A;Molecule type: nucleic acid
A;Residues: 1-1034 <THA>
A;Cross-references: UNIPROT:Q24714; EMBL:U26343
C;Genetics:
A;Gene: FlyBase:Dvir/para
A;Cross-references: FlyBase:FBgn0015214
C;Superfamily: sodium channel protein
C;Keywords: alternative splicing; duplication; transmembrane protein
F;306-329/Region: alternatively spliced segment i (exon 4) #status experimental
F;330-350/Region: alternatively spliced exon a #status experimental
F;538-545/Region: alternatively spliced segment b (exon 9) #status experimental
F;874-886/Region: alternatively spliced segment e (exon 12) #status experimental
F;887-896/Region: alternatively spliced segment f (exon 13) #status experimental
F;958-982/Region: alternatively spliced segment h (exon 14) #status experimental

  Query Match             60.7%;  Score 17;  DB 2;  Length 1034;
  Best Local Similarity   100.0%;  Pred. No. 3e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 VIGNLVVLNLFLALLLS 26
              |||||||||||||||||
Db        800 VIGNLVVLNLFLALLLS 816


RESULT 18
S60060
sodium channel alpha chain, exon d-containing splice form - fruit fly (Drosophila virili
C;Species: Drosophila virilis
C;Date: 24-Aug-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C;Accession: S60060
R;Thackeray, J.R.; Ganetzky, B.
Genetics 141, 203-214, 1995
A;Title: Conserved alternative splicing patterns and splicing signals in the Drosophila
A;Reference number: S60051; MUID:96042905; PMID:8536968
```

```
A;Accession: S60060
A;Status: nucleic acid sequence not shown
A;Molecule type: nucleic acid
A;Residues: 1-1034 <THA>
A;Cross-references: UNIPROT:Q24714; EMBL:U26343
C;Genetics:
A;Gene: FlyBase:Dvir/para
A;Cross-references: FlyBase:FBgn0015214
C;Superfamily: sodium channel protein
C;Keywords: alternative splicing; duplication; transmembrane protein
F;306-329/Region: alternatively spliced segment i (exon 4) #status experimental
F;330-350/Region: alternatively spliced exon a #status experimental
F;538-545/Region: alternatively spliced segment b (exon 9) #status experimental
F;874-886/Region: alternatively spliced segment e (exon 12) #status experimental
F;887-896/Region: alternatively spliced segment f (exon 13) #status experimental
F;958-982/Region: alternatively spliced segment h (exon 14) #status experimental

  Query Match             60.7%;  Score 17;  DB 2;  Length 1034;
  Best Local Similarity   100.0%;  Pred. No. 3e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 VIGNLVVLNLFLALLLS 26
              |||||||||||||||||
Db        800 VIGNLVVLNLFLALLLS 816


RESULT 19
S72467
sodium channel protein para-type alpha chain - German cockroach (strain CSMA) (fragment)
C;Species: Blattella germanica (German cockroach)
A;Variety: strain CSMA
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: S72467; S72487
R;Miyazaki, M.; Ohyama, K.; Dunlap, D.Y.; Matsumura, F.
submitted to the EMBL Data Library, September 1996
A;Description: Cloning and sequencing of the para-type sodium channel gene from suscepti
A;Reference number: S72467
A;Accession: S72467
A;Molecule type: mRNA
A;Residues: 1-1689 <MIY>
A;Cross-references: UNIPROT:Q93135; EMBL:U71083; NID:g1633647; PIDN:AAB82037.1; PID:g163
R;Miyazaki, M.; Ohyama, K.; Dunlap, D.Y.; Matsumura, F.
Mol. Gen. Genet. 252, 61-68, 1996
A;Title: Cloning and sequencing of the para-type sodium channel gene from susceptible an
A;Reference number: S72487; MUID:96397510; PMID:8804404
A;Accession: S72487
A;Molecule type: mRNA
A;Residues: 711-819 <MIW>
A;Cross-references: EMBL:U71083
C;Superfamily: sodium channel protein
C;Keywords: duplication; sodium channel; transmembrane protein

  Query Match             60.7%;  Score 17;  DB 2;  Length 1689;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 VIGNLVVLNLFLALLLS 26
              |||||||||||||||||
Db        781 VIGNLVVLNLFLALLLS 797


RESULT 20
A33299
sodium channel protein - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 21-Nov-1997
C;Accession: A33299
R;Loughney, K.; Kreber, R.; Ganetzky, B.
Cell 58, 1143-1154, 1989
A;Title: Molecular analysis of the para locus, a sodium channel gene in Drosophila.
A;Reference number: A33299; MUID:89376565; PMID:2550145
A;Accession: A33299
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1820 <LOU>
A;Cross-references: GB:M32078; GB:M24285
C;Genetics:
A;Gene: FlyBase:para
A;Cross-references: FlyBase:FBgn0003036
C;Superfamily: sodium channel protein
C;Keywords: duplication; phosphoprotein; transmembrane protein

  Query Match             60.7%;  Score 17;  DB 2;  Length 1820;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 VIGNLVVLNLFLALLLS 26
              |||||||||||||||||
Db       1004 VIGNLVVLNLFLALLLS 1020


RESULT 21
T30902
sodium channel SCAP1 alpha chain - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30902
R;Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.
DNA Cell Biol. 16, 347-356, 1997
A;Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit cDNA.
A;Reference number: Z20929; MUID:97238630; PMID:9115644
A;Accession: T30902
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1993 <DYE>
A;Cross-references: UNIPROT:P90670; EMBL:U66915; NID:g1842248; PID:g1842249; PIDN:AAC474
C;Superfamily: sodium channel protein

  Query Match             60.7%;  Score 17;  DB 2;  Length 1993;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GNLVVLNLFLALLLSSF 28
              |||||||||||||||||
Db        971 GNLVVLNLFLALLLSSF 987


RESULT 22
T43161
sodium channel protein TuNaI - sea squirt (Halocynthia roretzi)
C;Species: Halocynthia roretzi
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43161
R;Okamura, Y.; Ono, F.; Okagaki, R.; Chong, J.; Mandel, G.
Neuron 13, 937-948, 1994
A;Title: Neural expression of a sodium channel gene requires cell-specific interactions.
A;Reference number: Z22320; MUID:95033215; PMID:7946338
A;Accession: T43161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2049 <OKA>
A;Cross-references: UNIPROT:Q25150; EMBL:D17311; PIDN:BAA04133.1
C;Superfamily: sodium channel protein
C;Keywords: sodium channel; transmembrane protein

  Query Match             60.7%;  Score 17;  DB 2;  Length 2049;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GNLVVLNLFLALLLSSF 28
              |||||||||||||||||
Db       1009 GNLVVLNLFLALLLSSF 1025


RESULT 23
S72458
```

sodium channel protein para-type alpha chain - house fly (strain Cooper)
C;Species: Musca domestica (house fly)
A;Variety: strain Cooper
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
C;Accession: S72458
R;Williamson, M.S.; Martinez-Torres, D.; Hick, C.A.; Devonshire, A.L.
Mol. Gen. Genet. 252, 51-60, 1996
A;Title: Identification of mutations in the housefly para-type sodium channel gene assoc
A;Reference number: S72458; MUID:96397509; PMID:8804403
A;Accession: S72458
A;Molecule type: mRNA
A;Residues: 1-2108 <WIL>
A;Cross-references: UNIPROT:Q94615; EMBL:X96668
A;Experimental source: strain Cooper
C;Genetics:
A;Map position: 3
C;Superfamily: sodium channel protein
C;Keywords: alternative splicing; glycoprotein; phosphoprotein; sodium channel; transmem
F;302,314,332,967,1451,1470/Binding site: carbohydrate (Asn) (covalent) #status predicte
F;541,1208,1582/Binding site: phosphate (Ser) (covalent) #status predicted

  Query Match 60.7%; Score 17; DB 2; Length 2108;
  Best Local Similarity 100.0%; Pred. No. 5.5e-08;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 VIGNLVVLNLFLALLLS 26
|||||||||||||||||
Db 1010 VIGNLVVLNLFLALLLS 1026

RESULT 24
A25019
sodium channel protein I - rat
N;Alternate names: sodium channel protein A
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A25019; S40783; I84764
R;Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H
Nature 320, 188-192, 1986
A;Title: Existence of distinct sodium channel messenger RNAs in rat brain.
A;Reference number: A93377; MUID:86146901; PMID:3754035
A;Accession: A25019
A;Molecule type: mRNA
A;Residues: 1-2009 <NOD>
A;Cross-references: UNIPROT:P04774; GB:X03638; NID:g57216; PIDN:CAA27286.1; PID:g57217
A;Experimental source: brain
R;Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
Nucleic Acids Res. 19, 5673-5679, 1991
A;Title: Developmentally regulated alternative RNA splicing of rat brain sodium channel
A;Reference number: S40782; MUID:92051314; PMID:1658739
A;Accession: S40783
A;Molecule type: DNA
A;Residues: 177-253 <SAR>
R;Noda, M.; Numa, S.
J. Recept. Res. 7, 467-497, 1987
A;Title: Structure and function of sodium channel.
A;Reference number: I50536; MUID:87311395; PMID:2442385
A;Accession: I84764
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2009 <RES>
A;Cross-references: GB:M22253; NID:g1041088; PIDN:AAA79965.1; PID:g1041089
C;Superfamily: sodium channel protein
C;Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-g

  Query Match 57.1%; Score 16; DB 2; Length 2009;
  Best Local Similarity 100.0%; Pred. No. 4.6e-07;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 NLVVLNLFLALLLSSF 28
||||||||||||||||
Db 980 NLVVLNLFLALLLSSF 995

RESULT 25
JE0084
voltage-gated sodium channel alpha subunit - hydromedusa (Polyorchis penicillatus)
N;Alternate names: PpSCN 1
C;Species: Polyorchis penicillatus
C;Date: 11-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: JE0084
R;Spafford, J.D.; Spencer, A.N.; Gallin, W.J.
Biochem. Biophys. Res. Commun. 244, 772-780, 1998
A;Title: A putative voltage-gated sodium channel alpha subunit (PpSCN1) from the hydrozo
A;Reference number: JE0084; MUID:98205797; PMID:9535741
A;Accession: JE0084
A;Molecule type: mRNA
A;Residues: 1-1695 <SPA>
A;Cross-references: UNIPROT:O62604; GB:AF047380; NID:g3005563; PIDN:AAC38974.1; PID:g300
C;Comment: This protein is the only pore-forming alpha subunit available to account for
C;Superfamily: sodium channel protein
C;Keywords: glycoprotein
F;201,273,299,684,1065,1082,1089,1428/Binding site: carbohydrate (Asn) (covalent) #statu

  Query Match 50.0%; Score 14; DB 2; Length 1695;
  Best Local Similarity 100.0%; Pred. No. 3e-05;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 VVLNLFLALLLSSF 28
||||||||||||||
Db 704 VVLNLFLALLLSSF 717

Search completed: January 27, 2005, 17:52:44
Job time : 19 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:35:20 ; Search time 92.5 Seconds
(without alignments)
174.167 Million cell updates/sec

Title: US-10-608-584-13
Perfect score: 28
Sequence: 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	100.0	200	2	Q60464	Q60464 cricetulus
2	28	100.0	276	2	Q8UVC2	Q8uvc2 pagothenia
3	28	100.0	500	2	Q800U0	Q800u0 ictalurus p
4	28	100.0	1981	2	Q8IUJ6	Q8iuj6 homo sapien
5	28	100.0	2005	1	CIN2_HUMAN	Q99250 homo sapien
6	28	100.0	2005	1	CIN2_RAT	P04775 rattus norv
7	28	100.0	2007	2	Q9YGN7	Q9ygn7 cynops pyrr
8	28	100.0	2009	1	CIN1_HUMAN	P35498 homo sapien
9	25	89.3	472	2	Q800U4	Q800u4 ictalurus p
10	25	89.3	743	2	Q90Z26	Q90z26 sternopygus
11	25	89.3	751	2	Q90Z28	Q90z28 sternopygus
12	25	89.3	1717	2	Q90519	Q90519 fugu rubrip
13	25	89.3	1880	2	Q9IBF1	Q9ibf1 takifugu pa
14	25	89.3	1949	2	Q9DF53	Q9df53 brachydanio
15	25	89.3	1976	2	Q63541	Q63541 rattus norv
16	25	89.3	1978	1	CIN8_MOUSE	Q9wtu3 mus musculu
17	25	89.3	1978	2	O88420	O88420 rattus norv
18	25	89.3	1980	1	CIN8_HUMAN	Q9uqd0 homo sapien
19	25	89.3	1988	2	O88421	O88421 rattus norv
20	23	82.1	1977	2	Q15858	Q15858 homo sapien
21	23	82.1	1984	2	Q28644	Q28644 oryctolagus
22	23	82.1	1984	2	O08562	O08562 rattus norv
23	22	78.6	473	2	Q800T9	Q800t9 ictalurus p
24	22	78.6	488	2	Q800U1	Q800u1 ictalurus p
25	22	78.6	744	2	Q90Z27	Q90z27 sternopygus
26	22	78.6	1836	1	CIN4_HUMAN	P35499 homo sapien
27	22	78.6	1840	1	CIN4_RAT	P15390 rattus norv
28	22	78.6	1840	2	O70611	O70611 rattus norv
29	22	78.6	1841	2	Q9ER60	Q9er60 mus musculu
30	21	75.0	289	2	Q62204	Q62204 mus musculu
31	21	75.0	479	2	Q800U3	Q800u3 ictalurus p
32	21	75.0	488	2	Q800T8	Q800t8 ictalurus p
33	21	75.0	588	2	Q8JG67	Q8jg67 xenopus lae
34	21	75.0	1136	2	Q804F4	Q804f4 sternopygus
35	21	75.0	1951	1	CIN3_RAT	P08104 rattus norv
36	21	75.0	1951	2	Q9C007	Q9c007 homo sapien
37	21	75.0	1962	2	Q75RX9	Q75rx9 homo sapien
38	21	75.0	1962	2	BAD12085	Bad12085 homo sapi
39	21	75.0	1966	2	Q925G6	Q925g6 rattus norv
40	21	75.0	2000	1	CIN3_HUMAN	Q9ny46 homo sapien
41	21	75.0	2013	2	Q865W3	Q865w3 canis famil
42	21	75.0	2015	2	Q86UR3	Q86ur3 homo sapien
43	21	75.0	2015	2	Q8IZC9	Q8izc9 homo sapien
44	21	75.0	2015	2	Q96J69	Q96j69 homo sapien
45	21	75.0	2016	1	CIN5_HUMAN	Q14524 homo sapien
46	21	75.0	2016	2	Q75RY0	Q75ry0 homo sapien
47	21	75.0	2016	2	BAD12084	Bad12084 homo sapi
48	21	75.0	2019	1	CIN5_RAT	P15389 rattus norv
49	21	75.0	2019	2	Q9JJV9	Q9jjv9 mus musculu
50	21	75.0	2022	2	Q8WMP8	Q8wmp8 bos taurus
51	20	71.4	742	2	Q90Z29	Q90z29 sternopygus
52	19	67.9	1089	2	Q8IS97	Q8is97 varroa dest
53	19	67.9	1130	2	Q9XZC1	Q9xzc1 boophilus m
54	19	67.9	2215	2	Q86D77	Q86d77 varroa dest
55	18	64.3	1784	2	Q25377	Q25377 loligo opal
56	17	60.7	47	2	Q6TFL2	Q6tfl2 anopheles s
57	17	60.7	47	2	Q6V9Y7	Q6v9y7 anopheles f
58	17	60.7	47	2	Q6VE68	Q6ve68 anopheles c
59	17	60.7	47	2	Q6VE70	Q6ve70 anopheles c
60	17	60.7	47	2	Q7JNL8	Q7jnl8 heliothis v
61	17	60.7	47	2	AAR32092	Aar32092 anopheles
62	17	60.7	47	2	AAR32093	Aar32093 anopheles
63	17	60.7	47	2	AAR32094	Aar32094 anopheles
64	17	60.7	47	2	AAR32095	Aar32095 anopheles
65	17	60.7	47	2	AAR23795	Aar23795 anopheles
66	17	60.7	47	2	AAR23796	Aar23796 anopheles
67	17	60.7	124	2	Q86LC6	Q86lc6 meligethes
68	17	60.7	130	2	Q8MU84	Q8mu84 aedes aegyp
69	17	60.7	132	2	Q8IT45	Q8it45 pediculus h
70	17	60.7	132	2	Q8IT46	Q8it46 pediculus h
71	17	60.7	136	2	O45207	O45207 anopheles g
72	17	60.7	140	2	Q6KBA2	Q6kba2 ctenocephal
73	17	60.7	140	2	Q95VK8	Q95vk8 aphis gossy
74	17	60.7	140	2	Q95VK9	Q95vk9 aphis gossy
75	17	60.7	140	2	CAG30671	Cag30671 ctenoceph
76	17	60.7	142	2	O97167	O97167 culex pipie
77	17	60.7	162	2	Q710W0	Q710w0 frankliniel
78	17	60.7	162	2	Q710W1	Q710w1 frankliniel
79	17	60.7	162	2	CAC79234	Cac79234 franklini
80	17	60.7	162	2	CAC79235	Cac79235 franklini
81	17	60.7	162	2	CAC79236	Cac79236 franklini
82	17	60.7	220	2	Q95VP4	Q95vp4 aphis gossy
83	17	60.7	316	2	O18460	O18460 haematobia
84	17	60.7	329	2	O18461	O18461 haematobia
85	17	60.7	335	2	Q7JPG7	Q7jpg7 drosophila
86	17	60.7	340	2	Q7JPG6	Q7jpg6 drosophila
87	17	60.7	348	2	Q24726	Q24726 drosophila
88	17	60.7	508	2	Q800U2	Q800u2 ictalurus p
89	17	60.7	576	2	Q6DLU1	Q6dlu1 aedes aegyp
90	17	60.7	603	2	Q6DLT6	Q6dlt6 aedes albop
91	17	60.7	626	2	Q6DLT5	Q6dlt5 aedes albop
92	17	60.7	660	2	Q24717	Q24717 drosophila
93	17	60.7	689	2	Q24715	Q24715 drosophila
94	17	60.7	693	2	Q24712	Q24712 drosophila
95	17	60.7	701	2	Q24713	Q24713 drosophila
96	17	60.7	704	2	Q24716	Q24716 drosophila
97	17	60.7	706	2	Q24711	Q24711 drosophila
98	17	60.7	714	2	Q24714	Q24714 drosophila
99	17	60.7	1087	2	Q9XYM6	Q9xym6 leptinotars
100	17	60.7	1347	2	Q7PMT4	Q7pmt4 anopheles g

ALIGNMENTS

```
RESULT 1
Q60464
ID   Q60464      PRELIMINARY;      PRT;   200 AA.
AC   Q60464;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel alpha subunit (Fragment).
GN   Name=cho1;
OS   Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Cricetulus.
OX   NCBI_TaxID=10030;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=93235989; PubMed=7682773;
RA   Lalik P.H., Krafte D.S., Ciccarelli R.B.;
RT   "Characterization of endogenous Sodium channel gene expressed in
RT   chinese hamster ovary cells.";
RL   Am. J. Physiol. 264:803-809(1993).
DR   EMBL; M87541; AAA36979.1; -.
DR   PIR; I48108; I48108.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0006811; P:ion transport; IEA.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER     200    200
SQ   SEQUENCE   200 AA;  22676 MW;  A097916C0EE43458 CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 200;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||||||||
Db         45 CLTVFMMVMVIGNLVVLNLFLALLLSSF 72


RESULT 2
Q8UVC2
ID   Q8UVC2      PRELIMINARY;      PRT;   276 AA.
AC   Q8UVC2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Putative voltage-activated sodium channel alpha subunit
DE   (Fragment).
GN   Name=scn4a;
OS   Pagothenia bernacchii (Emerald rockcod) (Trematomus bernacchii).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC   Notothenioidei; Nototheniidae; Trematomus.
OX   NCBI_TaxID=40690;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RA   Moran O., Elia L.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF465250; AAL69973.1; -.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF06512; Na_trans_assoc; 1.
KW   Ionic channel.
FT   NON_TER       1      1
FT   NON_TER     276    276
SQ   SEQUENCE   276 AA;  30906 MW;  5660535780CA79B3 CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 276;
  Best Local Similarity   100.0%;  Pred. No. 5e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||||||||
Db         15 CLTVFMMVMVIGNLVVLNLFLALLLSSF 42


RESULT 3
Q800U0
ID   Q800U0      PRELIMINARY;      PRT;   500 AA.
AC   Q800U0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel 5 (Fragment).
OS   Ictalurus punctatus (Channel catfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC   Ictaluridae; Ictalurus.
OX   NCBI_TaxID=7998;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lu Y., Lopreato G.F., Zakon H.H.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY204536; AAO60424.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1      1
FT   NON_TER     500    500
SQ   SEQUENCE   500 AA;  56868 MW;  C7DE33040416FE3F CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 500;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||||||||
Db          6 CLTVFMMVMVIGNLVVLNLFLALLLSSF 33


RESULT 4
Q8IUJ6
ID   Q8IUJ6      PRELIMINARY;      PRT;  1981 AA.
AC   Q8IUJ6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel alpha 1 subunit.
GN   Name=SCN1A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Normal brain;
RA   Ouchida M., Ohmori I.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AB098335; BAC45228.1; -.
```

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DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008051; Na_channel1.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   InterPro; IPR000100; Ribonuclease_P.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01664; NACHANNEL1.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS00648; RIBONUCLEASE_P; UNKNOWN_1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1981 AA;  226201 MW;  B1D6946D6491B7AD CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 1981;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-17;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||||||||
Db        940 CLTVFMMVMVIGNLVVLNLFLALLLSSF 967


RESULT 5
CIN2_HUMAN
ID   CIN2_HUMAN     STANDARD;      PRT;  2005 AA.
AC   Q99250; Q14472; Q9BZC9; Q9BZD0;
DT   01-JUN-1994 (Rel. 29, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type II alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha
DE   subunit) (HBSC II).
GN   Name=SCN2A; Synonyms=SCN2A2, NAC2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=92390418; PubMed=1325650;
RA   Ahmed C.M., Ware D.H., Lee S.C., Patten C.D., Ferrer-Montiel A.V.,
RA   Schinder A.F., McPherson J.D., Wagner-Mcpherson C.B., Wasmuth J.J.,
RA   Evans G.A., Montal M.;
RT   "Primary structure, chromosomal localization, and functional
RT   expression of a voltage-gated sodium channel from human brain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:8220-8224(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX   MEDLINE=21142400; PubMed=11245985; DOI=10.1016/S0378-1119(00)00594-1;
RA   Kasai N., Fukushima K., Ueki Y., Prasad S., Nosakowski J.,
RA   Sugata K.-I., Sugata A., Nishizaki K., Meyer N.C., Smith R.J.H.;
RT   "Genomic structures of SCN2A and SCN3A - candidate genes for deafness
RT   at the DFNA16 locus.";
RL   Gene 264:113-122(2001).
RN   [3]
RP   SEQUENCE OF 1-89 FROM N.A.
RA   Lu C.-M., Eichelberger J.S., Beckman M.L., Schade S.D., Brown G.B.;
RT   "Isolation of the 5'-flanking region for human brain sodium channel
RT   subtype II alpha-Subunit (SCN2A).";
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1702-2005 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92275082; PubMed=1317301;
RA   Lu C.-M., Han J., Rado T.A., Brown G.B.;
RT   "Differential expression of two sodium channel subtypes in human
RT   brain.";
RL   FEBS Lett. 303:53-58(1992).
RN   [5]
RP   SEQUENCE OF 1702-1772 FROM N.A.
RX   MEDLINE=91110524; PubMed=1846440;
RA   Han J., Lu C.-M., Brown G.B., Rado T.A.;
RT   "Direct amplification of a single dissected chromosomal segment by
RT   polymerase chain reaction: a human brain sodium channel gene is on
RT   chromosome 2q22-q23.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:335-339(1991).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Adult, 6A;
CC         IsoId=Q99250-1; Sequence=Displayed;
CC       Name=2; Synonyms=Neonatal, 6N;
CC         IsoId=Q99250-2; Sequence=VSP_001032;
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M94055; AAA18895.1; -.
DR   EMBL; AF059683; AAC14574.1; -.
DR   EMBL; AF327246; AAG53413.1; -.
DR   EMBL; AF327226; AAG53413.1; JOINED.
DR   EMBL; AF327227; AAG53413.1; JOINED.
DR   EMBL; AF327228; AAG53413.1; JOINED.
DR   EMBL; AF327229; AAG53413.1; JOINED.
DR   EMBL; AF327230; AAG53413.1; JOINED.
DR   EMBL; AF327231; AAG53413.1; JOINED.
DR   EMBL; AF327232; AAG53413.1; JOINED.
DR   EMBL; AF327233; AAG53413.1; JOINED.
DR   EMBL; AF327234; AAG53413.1; JOINED.
DR   EMBL; AF327235; AAG53413.1; JOINED.
DR   EMBL; AF327236; AAG53413.1; JOINED.
DR   EMBL; AF327237; AAG53413.1; JOINED.
DR   EMBL; AF327238; AAG53413.1; JOINED.
DR   EMBL; AF327239; AAG53413.1; JOINED.
DR   EMBL; AF327240; AAG53413.1; JOINED.
DR   EMBL; AF327241; AAG53413.1; JOINED.
DR   EMBL; AF327242; AAG53413.1; JOINED.
DR   EMBL; AF327243; AAG53413.1; JOINED.
DR   EMBL; AF327244; AAG53413.1; JOINED.
DR   EMBL; AF327245; AAG53413.1; JOINED.
DR   EMBL; AF327246; AAG53412.1; -.
DR   EMBL; AF327226; AAG53412.1; JOINED.
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DR   EMBL; AF327227; AAG53412.1; JOINED.
DR   EMBL; AF327228; AAG53412.1; JOINED.
DR   EMBL; AF327229; AAG53412.1; JOINED.
DR   EMBL; AF327230; AAG53412.1; JOINED.
DR   EMBL; AF327231; AAG53412.1; JOINED.
DR   EMBL; AF327232; AAG53412.1; JOINED.
DR   EMBL; AF327233; AAG53412.1; JOINED.
DR   EMBL; AF327234; AAG53412.1; JOINED.
DR   EMBL; AF327235; AAG53412.1; JOINED.
DR   EMBL; AF327236; AAG53412.1; JOINED.
DR   EMBL; AF327237; AAG53412.1; JOINED.
DR   EMBL; AF327238; AAG53412.1; JOINED.
DR   EMBL; AF327239; AAG53412.1; JOINED.
DR   EMBL; AF327240; AAG53412.1; JOINED.
DR   EMBL; AF327241; AAG53412.1; JOINED.
DR   EMBL; AF327242; AAG53412.1; JOINED.
DR   EMBL; AF327243; AAG53412.1; JOINED.
DR   EMBL; AF327244; AAG53412.1; JOINED.
DR   EMBL; AF327245; AAG53412.1; JOINED.
DR   EMBL; X65361; CAA46438.1; ALT_SEQ.
DR   EMBL; M91804; -; NOT_ANNOTATED_CDS.
DR   EMBL; M55662; AAB65854.2; -.
DR   HSSP; P04775; 1BYY.
DR   Genew; HGNC:10588; SCN2A2.
DR   MIM; 601219; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; TAS.
DR   GO; GO:0006814; P:sodium ion transport; TAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   REPEAT      111    456       I.
FT   REPEAT      741   1013       II.
FT   REPEAT     1190   1504       III.
FT   REPEAT     1513   1811       IV.
FT   TRANSMEM    125    148       S1 of repeat I.
FT   TRANSMEM    157    176       S2 of repeat I.
FT   TRANSMEM    190    208       S3 of repeat I.
FT   TRANSMEM    215    234       S4 of repeat I.
FT   TRANSMEM    251    274       S5 of repeat I.
FT   TRANSMEM    402    427       S6 of repeat I.
FT   TRANSMEM    754    778       S1 of repeat II.
FT   TRANSMEM    790    813       S2 of repeat II.
FT   TRANSMEM    822    841       S3 of repeat II.
FT   TRANSMEM    848    867       S4 of repeat II.
FT   TRANSMEM    884    904       S5 of repeat II.
FT   TRANSMEM    958    983       S6 of repeat II.
FT   TRANSMEM   1204   1227       S1 of repeat III.
FT   TRANSMEM   1241   1266       S2 of repeat III.
FT   TRANSMEM   1273   1294       S3 of repeat III.
FT   TRANSMEM   1299   1320       S4 of repeat III.
FT   TRANSMEM   1340   1367       S5 of repeat III.
FT   TRANSMEM   1447   1473       S6 of repeat III.
FT   TRANSMEM   1527   1550       S1 of repeat IV.
FT   TRANSMEM   1562   1585       S2 of repeat IV.
FT   TRANSMEM   1592   1615       S3 of repeat IV.
FT   TRANSMEM   1626   1647       S4 of repeat IV.
FT   TRANSMEM   1663   1685       S5 of repeat IV.
FT   TRANSMEM   1752   1776       S6 of repeat IV.
FT   DOMAIN     1905   1934       IQ.
FT   CARBOHYD    212    212       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    285    285       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    291    291       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    297    297       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    303    303       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    340    340       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    604    604       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    624    624       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    883    883       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1055   1055       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1072   1072       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1136   1136       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1368   1368       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1382   1382       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1393   1393       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1778   1778       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    209    209       D -> N (in isoform 2).
FT                                /FTId=VSP_001032.
FT   CONFLICT    524    524       R -> L (in Ref. 1).

  Query Match             100.0%;  Score 28;  DB 1;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-17;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||||||||
Db        959 CLTVFMMVMVIGNLVVLNLFLALLLSSF 986


RESULT 6
CIN2_RAT
ID   CIN2_RAT       STANDARD;      PRT;  2005 AA.
AC   P04775;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Sodium channel protein type II alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha
DE   subunit).
GN   Name=Scn2a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86146901; PubMed=3754035;
RA   Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M.,
RA   Takahashi H., Numa S.;
RT   "Existence of distinct sodium channel messenger RNAs in rat brain.";
RL   Nature 320:188-192(1986).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X03639; CAA27287.1; -.
DR   PDB; 1BYY; NMR; A=1474-1526.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   3D-structure; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   REPEAT      111    456       I.
FT   REPEAT      741   1013       II.
FT   REPEAT     1190   1504       III.
FT   REPEAT     1513   1811       IV.
FT   TRANSMEM    125    148       S1 of repeat I.
FT   TRANSMEM    157    176       S2 of repeat I.
FT   TRANSMEM    190    208       S3 of repeat I.
FT   TRANSMEM    215    234       S4 of repeat I.
FT   TRANSMEM    251    274       S5 of repeat I.
FT   TRANSMEM    402    427       S6 of repeat I.
FT   TRANSMEM    754    778       S1 of repeat II.
FT   TRANSMEM    790    813       S2 of repeat II.
FT   TRANSMEM    822    841       S3 of repeat II.
FT   TRANSMEM    848    867       S4 of repeat II.
FT   TRANSMEM    884    904       S5 of repeat II.
FT   TRANSMEM    958    983       S6 of repeat II.
FT   TRANSMEM   1204   1227       S1 of repeat III.
FT   TRANSMEM   1241   1266       S2 of repeat III.
FT   TRANSMEM   1273   1294       S3 of repeat III.
FT   TRANSMEM   1299   1320       S4 of repeat III.
FT   TRANSMEM   1340   1367       S5 of repeat III.
FT   TRANSMEM   1447   1473       S6 of repeat III.
FT   TRANSMEM   1527   1550       S1 of repeat IV.
FT   TRANSMEM   1562   1585       S2 of repeat IV.
FT   TRANSMEM   1592   1615       S3 of repeat IV.
FT   TRANSMEM   1626   1647       S4 of repeat IV.
FT   TRANSMEM   1663   1685       S5 of repeat IV.
FT   TRANSMEM   1752   1776       S6 of repeat IV.
FT   DOMAIN     1905   1934       IQ.
FT   CARBOHYD    212    212       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    285    285       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    291    291       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    297    297       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    303    303       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    340    340       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    604    604       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    624    624       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    883    883       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1055   1055       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1072   1072       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1136   1136       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1368   1368       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1382   1382       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1393   1393       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   2005 AA;  227872 MW;  861BE583D79F8324 CRC64;

  Query Match           100.0%;  Score 28;  DB 1;  Length 2005;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-17;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
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Db        959 CLTVFMMVMVIGNLVVLNLFLALLLSSF 986
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RESULT 7
Q9YGN7
ID   Q9YGN7      PRELIMINARY;      PRT;  2007 AA.
AC   Q9YGN7;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-dependent sodium channel.
OS   Cynops pyrrhogaster (Japanese common newt).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX   NCBI_TaxID=8330;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RA   Hirota K., Kaneko Y., Matsumoto G., Hanyu Y.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AF123593; AAD17315.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   2007 AA;  228398 MW;  013E9B9EC9C294C9 CRC64;

  Query Match           100.0%;  Score 28;  DB 2;  Length 2007;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-17;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||||||||
Db        957 CLTVFMMVMVIGNLVVLNLFLALLLSSF 984


RESULT 8
CIN1_HUMAN
ID   CIN1_HUMAN     STANDARD;      PRT;  2009 AA.
AC   P35498; Q16172; Q96LA3; Q9C008;
DT   01-JUN-1994 (Rel. 29, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type I alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.1) (Sodium channel protein, brain I alpha
DE   subunit).
GN   Name=SCN1A; Synonyms=SCN1, NAC1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS GEFS+2 MET-875 AND
RP   HIS-1648.
RX   MEDLINE=20206553; PubMed=10742094;
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RA   Escayg A., MacDonald B.T., Meisler M.H., Baulac S., Huberfeld G.,
RA   An-Gourfinkel I., Brice A., LeGuern E., Moulard B., Chaigne D.,
RA   Buresi C., Malafosse A.;
RT   "Mutations of SCN1A, encoding a neuronal sodium channel, in two
RT   families with GEFS+2.";
RL   Nat. Genet. 24:343-345(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RA   Jeong S.-Y., Goto J., Kanazawa I.;
RT   "Cloning of cDNA for human voltage-gated sodium channel alpha subunit,
RT   SCN1A.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Brain;
RA   Sugawara T., Mazaki E.M., Yamakawa K.;
RT   "Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1)
RT   mRNA.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT THR-1067.
RA   Ouchida M., Ohmori I.;
RT   "Isoforms of human sodium channel SCN1A gene.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 1335-1428 FROM N.A.
RX   MEDLINE=94340991; PubMed=8062593;
RA   Malo M.S., Blanchard B.J., Andresen J.M., Srivastava K., Chen X.N.,
RA   Li X., Jabs E.W., Korenberg J.R., Ingram V.M.;
RT   "Localization of a putative human brain sodium channel gene (SCN1A) to
RT   chromosome band 2q24.";
RL   Cytogenet. Cell Genet. 67:178-186(1994).
RN   [6]
RP   SEQUENCE OF 1518-1940 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92275082; PubMed=1317301;
RA   Lu C.-M., Han J., Rado T.A., Brown G.B.;
RT   "Differential expression of two sodium channel subtypes in human
RT   brain.";
RL   FEBS Lett. 303:53-58(1992).
RN   [7]
RP   VARIANTS GEFS+2 VAL-188; LEU-1353 AND MET-1656.
RX   MEDLINE=21152274; PubMed=11254444;
RA   Wallace R.H., Scheffer I.E., Barnett S., Richards M., Dibbens L.,
RA   Desai R.R., Lerman-Sagie T., Lev D., Mazarib A., Brand N.,
RA   Ben-Zeev B., Goikhman I., Singh R., Kremmidiotis G., Gardner A.,
RA   Sutherland G.R., George A.L. Jr., Mulley J.C., Berkovic S.F.;
RT   "Neuronal sodium-channel alpha1-subunit mutations in generalized
RT   epilepsy with febrile seizures plus.";
RL   Am. J. Hum. Genet. 68:859-865(2001).
RN   [8]
RP   VARIANT GEFS+2 ARG-1204.
RX   MEDLINE=21152275; PubMed=11254445;
RA   Escayg A., Heils A., MacDonald B.T., Haug K., Sander T., Meisler M.H.;
RT   "A novel SCN1A mutation associated with generalized epilepsy with
RT   febrile seizures plus -- and prevalence of variants in patients with
RT   epilepsy.";
RL   Am. J. Hum. Genet. 68:866-873(2001).
RN   [9]
RP   VARIANT SMEI PHE-986.
RX   MEDLINE=21257503; PubMed=11359211;
RA   Claes L., Del-Favero J., Ceulemans B., Lagae L., Van Broeckhoven C.,
RA   De Jonghe P.;
RT   "De novo mutations in the sodium-channel gene SCN1A cause severe
RT   myoclonic epilepsy of infancy.";
RL   Am. J. Hum. Genet. 68:1327-1332(2001).
RN   [10]
RP   VARIANT GEFS+2 THR-1270.
RX   MEDLINE=21630138; PubMed=11756608;
RA   Abou-Khalil B., Ge Q., Desai R., Ryther R., Bazyk A., Bailey R.,
RA   Haines J.L., Sutcliffe J.S., George A.L. Jr.;
RT   "Partial and generalized epilepsy with febrile seizures plus and a
RT   novel SCN1A mutation.";
RL   Neurology 57:2265-2272(2001).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=P35498-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P35498-2; Sequence=VSP_001031;
CC         Note=No experimental confirmation available;
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- DISEASE: Defects in SCN1A are the cause of generalized epilepsy
CC       with febrile seizures plus type 2 (GEFS+2) [MIM:604233]. This
CC       autosomal dominant disorder is characterized by febrile seizures
CC       in children and afebrile seizures in adults. Penetrance is
CC       incomplete and a large intrafamilial variability of the phenotype
CC       is observed.
CC   -!- DISEASE: Defects in SCN1A are a cause of severe myoclonic epilepsy
CC       in infancy (SMEI) [MIM:607208], a severe form of generalized
CC       epilepsy with febrile seizures. SMEI is a rare disorder
CC       characterized by normal development before onset, seizures
CC       beginning in the first year of life in the form of generalized or
CC       unilateral febrile clonic seizures, secondary appearance of
CC       myoclonic seizures, and occasionally partial seizures. It is
CC       associated with ataxia, slowed psychomotor development, and mental
CC       decline.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF225985; AAK00217.1; -.
DR   EMBL; AY043484; AAK95360.1; -.
DR   EMBL; AB093548; BAC21101.1; -.
DR   EMBL; AB093549; BAC21102.1; -.
DR   EMBL; S71446; AAB31605.1; -.
DR   EMBL; X65362; CAA46439.1; -.
DR   EMBL; M91803; -; NOT_ANNOTATED_CDS.
DR   PIR; I52964; I52964.
DR   PIR; S29184; S29184.
DR   HSSP; P04775; 1BYY.
DR   Genew; HGNC:10585; SCN1A.
DR   MIM; 182389; -.
DR   MIM; 604233; -.
DR   MIM; 607208; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; NAS.
DR   GO; GO:0006814; P:sodium ion transport; NAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008051; Na_channel1.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
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DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01664; NACHANNEL1.
DR   PROSITE; PS50096; IQ; FALSE_NEG.
KW   Alternative splicing; Disease mutation; Epilepsy; Glycoprotein;
KW   Ion transport; Ionic channel; Multigene family; Polymorphism; Repeat;
KW   Sodium channel; Transmembrane; Voltage-gated channel.
FT   REPEAT      110    454       I.
FT   REPEAT      750   1022       II.
FT   REPEAT     1200   1514       III.
FT   REPEAT     1523   1821       IV.
FT   TRANSMEM    124    147       S1 of repeat I (By similarity).
FT   TRANSMEM    156    175       S2 of repeat I (By similarity).
FT   TRANSMEM    189    207       S3 of repeat I (By similarity).
FT   TRANSMEM    214    233       S4 of repeat I (By similarity).
FT   TRANSMEM    250    273       S5 of repeat I (By similarity).
FT   TRANSMEM    400    425       S6 of repeat I (By similarity).
FT   TRANSMEM    763    787       S1 of repeat II (By similarity).
FT   TRANSMEM    799    822       S2 of repeat II (By similarity).
FT   TRANSMEM    831    850       S3 of repeat II (By similarity).
FT   TRANSMEM    857    876       S4 of repeat II (By similarity).
FT   TRANSMEM    893    913       S5 of repeat II (By similarity).
FT   TRANSMEM    967    992       S6 of repeat II (By similarity).
FT   TRANSMEM   1214   1237       S1 of repeat III (By similarity).
FT   TRANSMEM   1251   1276       S2 of repeat III (By similarity).
FT   TRANSMEM   1283   1304       S3 of repeat III (By similarity).
FT   TRANSMEM   1309   1330       S4 of repeat III (By similarity).
FT   TRANSMEM   1350   1377       S5 of repeat III (By similarity).
FT   TRANSMEM   1457   1483       S6 of repeat III (By similarity).
FT   TRANSMEM   1537   1560       S1 of repeat IV (By similarity).
FT   TRANSMEM   1572   1595       S2 of repeat IV (By similarity).
FT   TRANSMEM   1602   1625       S3 of repeat IV (By similarity).
FT   TRANSMEM   1636   1657       S4 of repeat IV (By similarity).
FT   TRANSMEM   1673   1695       S5 of repeat IV (By similarity).
FT   TRANSMEM   1762   1786       S6 of repeat IV (By similarity).
FT   CARBOHYD    211    211       N-linked (GlcNAc. . .) (Potential).

  Query Match             100.0%;  Score 28;  DB 1;  Length 2009;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-17;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||||||||
Db        968 CLTVFMMVMVIGNLVVLNLFLALLLSSF 995


RESULT 9
Q800U4
ID   Q800U4      PRELIMINARY;      PRT;   472 AA.
AC   Q800U4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel 1 (Fragment).
OS   Ictalurus punctatus (Channel catfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC   Ictaluridae; Ictalurus.
OX   NCBI_TaxID=7998;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lu Y., Lopreato G.F., Zakon H.H.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY204532; AAO60420.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1      1
FT   NON_TER     472    472
SQ   SEQUENCE   472 AA;  53917 MW;  3DD68F4EAE484FAB CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-15;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||||
Db          9 VFMMVMVIGNLVVLNLFLALLLSSF 33


RESULT 10
Q90Z26
ID   Q90Z26      PRELIMINARY;      PRT;   743 AA.
AC   Q90Z26;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel 5 (Fragment).
OS   Sternopygus macrurus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC   Sternopygidae; Sternopygus.
OX   NCBI_TaxID=77841;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21310016; PubMed=11416226;
RA   Lopreato G.F., Lu Y., Southwell A., Atkinson N.S., Hillis D.M.,
RA   Wilcox T.P., Zakon H.H.;
RT   "Evolution and divergence of sodium channel genes in vertebrates.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7588-7592(2001).
DR   EMBL; AF378143; AAK55441.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 2.
DR   Pfam; PF06512; Na_trans_assoc; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1      1
FT   NON_TER     743    743
SQ   SEQUENCE   743 AA;  84781 MW;  F2429665544CAB0C CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 743;
  Best Local Similarity   100.0%;  Pred. No. 7e-15;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||||
Db        182 VFMMVMVIGNLVVLNLFLALLLSSF 206


RESULT 11
Q90Z28
ID   Q90Z28      PRELIMINARY;      PRT;   751 AA.
AC   Q90Z28;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel 3 (Fragment).
OS   Sternopygus macrurus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC   Sternopygidae; Sternopygus.
OX   NCBI_TaxID=77841;
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RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21310016; PubMed=11416226;
RA   Lopreato G.F., Lu Y., Southwell A., Atkinson N.S., Hillis D.M.,
RA   Wilcox T.P., Zakon H.H.;
RT   "Evolution and divergence of sodium channel genes in vertebrates.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7588-7592(2001).
DR   EMBL; AF378141; AAK55439.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 2.
DR   Pfam; PF06512; Na_trans_assoc; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1      1
FT   NON_TER     751    751
SQ   SEQUENCE   751 AA;  84598 MW;  CBFE6162E90A76FC CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 751;
  Best Local Similarity   100.0%;  Pred. No. 7e-15;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||||
Db        182 VFMMVMVIGNLVVLNLFLALLLSSF 206


RESULT 12
Q90519
ID   Q90519      PRELIMINARY;      PRT;  1717 AA.
AC   Q90519;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel alpha subunit (Fragment).
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Nakazawa A.;
RL   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; D37977; BAA07195.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008054; Na_channel8.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01667; NACHANNEL8.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
FT   NON_TER       1      1
SQ   SEQUENCE   1717 AA;  195413 MW;  067D566B3FA41C8D CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 1717;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-14;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||||
Db        721 VFMMVMVIGNLVVLNLFLALLLSSF 745


RESULT 13
Q9IBF1
ID   Q9IBF1      PRELIMINARY;      PRT;  1880 AA.
AC   Q9IBF1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel.
OS   Takifugu pardalis (Panther puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=98921;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=20090650; PubMed=10623632;
RA   Yotsu-Yamashita M., Nishimori K., Nitanai Y., Isemura M., Sugimoto A.,
RA   Yasumoto T.;
RT   "Binding properties of 3H-PbTx-3 and 3H-saxitoxin to brain membranes
RT   and to skeletal muscle membranes of puffer fish Fugu pardalis, and the
RT   primary structure of a voltage-gated Na+ channel alpha-subunit (fMNa1)
RT   from skeletal muscle of F. pardalis.";
RL   Biochem. Biophys. Res. Commun. 267:403-412(2000).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AB030482; BAA90398.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1880 AA;  212084 MW;  406483C6C3D43E02 CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 1880;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-14;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
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Db        803 VFMMVMVIGNLVVLNLFLALLLSSF 827


RESULT 14
Q9DF53
ID   Q9DF53      PRELIMINARY;      PRT;  1949 AA.
AC   Q9DF53;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel protein Scn8a.
GN   Name=scn8a;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=oregon;
RA   Tsai C.-W., Tseng J.-J., Horng J.-F., Wu J.-L., Tsay H.-J.;
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AF297658; AAG18440.1; -.
DR   HSSP; P04775; 1BYY.
DR   ZFIN; ZDB-GENE-000828-1; scn8a.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008054; Na_channel8.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01667; NACHANNEL8.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1949 AA;  221760 MW;  6BCA69664BDC7BC3 CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 1949;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-14;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||||
Db        925 VFMMVMVIGNLVVLNLFLALLLSSF 949


RESULT 15
Q63541
ID   Q63541      PRELIMINARY;      PRT;  1976 AA.
AC   Q63541;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel protein 6.
GN   Name=SCP6;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=95271284; PubMed=7751906;
RA   Schaller K.L., Krzemien D.M., Yarowsky P.J., Krueger B.K.,
RA   Caldwell J.H.;
RT   "A novel, abundant sodium channel expressed in neurons and glia.";
RL   J. Neurosci. 15:3231-3242(1995).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; L39018; AAC42059.1; -.
DR   PIR; I56555; I56555.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR000183; Decarbxylse2.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008054; Na_channel8.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01667; NACHANNEL8.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
DR   PROSITE; PS00878; ODR_DC_2_1; UNKNOWN_1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1976 AA;  225227 MW;  B6949327A47FA88A CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 1976;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-14;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||||
Db        952 VFMMVMVIGNLVVLNLFLALLLSSF 976


RESULT 16
CIN8_MOUSE
ID   CIN8_MOUSE     STANDARD;      PRT;  1978 AA.
AC   Q9WTU3; Q60828; Q60858; Q62449;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type VIII alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.6).
GN   Name=Scn8a; Synonyms=Nbna1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RC   STRAIN=C57BL/6J;
RX   MEDLINE=99047535; PubMed=9828131;
RA   Plummer N.W., Galt J., Jones J.M., Burgess D.L., Sprunger L.K.,
RA   Kohrman D.C., Meisler M.H.;
RT   "Exon organization, coding sequence, physical mapping, and polymorphic
RT   intragenic markers for the human neuronal sodium channel gene SCN8A.";
RL   Genomics 54:287-296(1998).
RN   [2]
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RP   SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND DISEASE.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=95400328; PubMed=7670495;
RA   Burgess D.L., Kohrman D.C., Galt J., Plummer N.W., Jones J.M.,
RA   Spear B., Meisler M.H.;
RT   "Mutation of a new sodium channel gene, Scn8a, in the mouse mutant
RT   'motor endplate disease'.";
RL   Nat. Genet. 10:461-465(1995).
RN   [3]
RP   SEQUENCE OF 93-205 FROM N.A., AND DISEASE.
RC   STRAIN=129/Sv; TISSUE=Brain;
RX   MEDLINE=96291923; PubMed=8663325;
RA   Kohrman D.C., Harris J.B., Meisler M.H.;
RT   "Mutation detection in the med and medJ alleles of the sodium channel
RT   Scn8a. Unusual splicing due to a minor class AT-AC intron.";
RL   J. Biol. Chem. 271:17576-17581(1996).
RN   [4]
RP   SEQUENCE OF 1411-1686 FROM N.A.
RA   Fan Z., Kyle J.W., Makielski J.C.;
RT   "A putative novel Na channel alpha subunit cDNA isolated from mouse
RT   NB2a neuroblastoma cells.";
RL   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   ALTERNATIVE SPLICING (ISOFORMS 1; 4 AND 5).
RC   TISSUE=Brain, and Fetal brain;
RX   MEDLINE=97442476; PubMed=9295353;
RA   Plummer N.W., McBurney M.W., Meisler M.H.;
RT   "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT   two-domain protein in fetal brain and non-neuronal cells.";
RL   J. Biol. Chem. 272:24008-24015(1997).
RN   [6]
RP   VARIANT MEDJO THR-1317, AND VARIANT LEU-5.
RC   STRAIN=DBA/2WyDi;
RX   MEDLINE=96424513; PubMed=8815882;
RA   Kohrman D.C., Smith M.R., Goldin A.L., Harris J., Meisler M.H.;
RT   "A missense mutation in the sodium channel Scn8a is responsible for
RT   cerebellar ataxia in the mouse mutant jolting.";
RL   J. Neurosci. 16:5993-5999(1996).
RN   [7]
RP   DISEASE.
RX   MEDLINE=21423786; PubMed=11532991;
RA   De Repentigny Y., Cote P.D., Pool M., Bernier G., Girard S.,
RA   Vidal S.M., Kothary R.;
RT   "Pathological and genetic analysis of the degenerating muscle (dmu)
RT   mouse: a new allele of Scn8a.";
RL   Hum. Mol. Genet. 10:1819-1827(2001).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=5;
CC       Name=1; Synonyms=18A;
CC         IsoId=Q9WTU3-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q9WTU3-2; Sequence=VSP_050594;
CC       Name=3;
CC         IsoId=Q9WTU3-3; Sequence=VSP_050595;
CC       Name=4; Synonyms=18N;
CC         IsoId=Q9WTU3-4; Sequence=VSP_050596, VSP_050597;
CC       Name=5;
CC         IsoId=Q9WTU3-5; Sequence=VSP_050598;
CC   -!- TISSUE SPECIFICITY: Expressed in brain, cerebellum and spinal
CC       cord.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- DISEASE: Defects in Scn8a are the cause of motor endplate disease
CC       (med). Med is a recessive neuromuscular disorder that is
CC       characterized by lack of signal transmission at the neuromuscular
CC       junction, excess preterminal arborization and degeneration of
CC       cerebellar Purkinje cells. It produces early onset progressive
CC       paralysis of hind limbs, severe muscle atrophy and juvenile
CC       lethality.
CC   -!- DISEASE: Defects in Scn8a are the cause of the jolting mutant
CC       (medjo), a mild form of motor endplate disease which is
CC       characterized by the absence of spontaneous, regular, simple
CC       discharges from Purkinje cells. After 3 weeks of age, jolting mice
CC       are unsteady and have wide-based gait and a rhythmical tremor of
CC       head and neck induced by attempted movement.
CC   -!- DISEASE: Defects in Scn8a are a cause of degenerating muscle
CC       (dmu). Dmu is an autosomal recessive neuromuscular disorder that
CC       is characterized by skeletal and cardiac muscle degeneration. It
CC       produces early onset progressive loss of mobility of the hind
CC       limbs and subsequent lethality in the first month of life.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF049617; AAD20438.1; -.
DR   EMBL; U26707; AAC52242.1; -.
DR   EMBL; U59964; AAC52708.1; -.
DR   EMBL; U59963; AAC52708.1; JOINED.
DR   EMBL; U23158; AAA65599.1; -.
DR   HSSP; P04775; 1BYY.
DR   MGD; MGI:103169; Scn8a.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IC.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; NAS.
DR   GO; GO:0007628; P:adult walking behavior; IMP.
DR   GO; GO:0006814; P:sodium ion transport; NAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008054; Na_channel8.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01667; NACHANNEL8.
DR   PROSITE; PS50096; IQ; 1.
KW   Alternative splicing; ATP-binding; Disease mutation; Glycoprotein;
KW   Ion transport; Ionic channel; Multigene family; Polymorphism; Repeat;
KW   Sodium channel; Transmembrane; Voltage-gated channel.
FT   REPEAT      114    442       I.
FT   REPEAT      733   1005       II.
FT   REPEAT     1178   1493       III.
FT   REPEAT     1502   1799       IV.
FT   TRANSMEM    128    151       S1 of repeat I.
FT   TRANSMEM    160    179       S2 of repeat I.
FT   TRANSMEM    193    211       S3 of repeat I.
FT   TRANSMEM    218    237       S4 of repeat I.
FT   TRANSMEM    253    277       S5 of repeat I.
FT   TRANSMEM    388    413       S6 of repeat I.
FT   TRANSMEM    746    770       S1 of repeat II.
FT   TRANSMEM    782    805       S2 of repeat II.
FT   TRANSMEM    814    833       S3 of repeat II.
FT   TRANSMEM    840    860       S4 of repeat II.
FT   TRANSMEM    876    896       S5 of repeat II.
FT   TRANSMEM    950    975       S6 of repeat II.
FT   TRANSMEM   1192   1215       S1 of repeat III.
FT   TRANSMEM   1229   1254       S2 of repeat III.
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FT   TRANSMEM   1261   1282       S3 of repeat III.
FT   TRANSMEM   1287   1308       S4 of repeat III.
FT   TRANSMEM   1328   1349       S5 of repeat III.
FT   TRANSMEM   1436   1462       S6 of repeat III.
FT   TRANSMEM   1516   1539       S1 of repeat IV.
FT   TRANSMEM   1551   1574       S2 of repeat IV.
FT   TRANSMEM   1581   1604       S3 of repeat IV.
FT   TRANSMEM   1615   1636       S4 of repeat IV.
FT   TRANSMEM   1652   1674       S5 of repeat IV.
FT   TRANSMEM   1740   1764       S6 of repeat IV.
FT   DOMAIN     1893   1922       IQ.
FT   NP_BIND     891    898       ATP (Potential).
FT   CARBOHYD    215    215       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    289    289       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    295    295       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    326    326       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    544    544       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    640    640       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    875    875       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1045   1045       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1062   1062       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1089   1089       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1356   1356       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1370   1370       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1381   1381       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1766   1766       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    428    673       Missing (in isoform 2).
FT                                /FTId=VSP_050594.
FT   VARSPLIC    664    664       E -> EVKIDKAATDS (in isoform 3).
FT                                /FTId=VSP_050595.
FT   VARSPLIC   1273   1280       SLVSLIAN -> PLSLSGLI (in isoform 4).

  Query Match             89.3%;  Score 25;  DB 1;  Length 1978;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-14;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||||
Db        954 VFMMVMVIGNLVVLNLFLALLLSSF 978


RESULT 17
O88420
ID   O88420      PRELIMINARY;      PRT;  1978 AA.
AC   O88420;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel rPN4.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dorsal root ganglia;
RX   MEDLINE=98264329; PubMed=9603190;
RA   Dietrich P.S., McGivern J.G., Delgado S.G., Koch B.D., Eglen R.M.,
RA   Hunter J.C., Sangameswaran L.;
RT   "Functional analysis of a voltage-gated sodium channel and its splice
RT   variant from rat dorsal root ganglia.";
RL   J. Neurochem. 70:2262-2272(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AF049239; AAC26014.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR000183; Decarbxylse2.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008054; Na_channel8.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01667; NACHANNEL8.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
DR   PROSITE; PS00878; ODR_DC_2_1; UNKNOWN_1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1978 AA;  225157 MW;  9160843C5935B88B CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 1978;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-14;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||||
Db        954 VFMMVMVIGNLVVLNLFLALLLSSF 978


RESULT 18
CIN8_HUMAN
ID   CIN8_HUMAN     STANDARD;      PRT;  1980 AA.
AC   Q9UQD0; O95788; Q9NYX2; Q9UPB2;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type VIII alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.6).
GN   Name=SCN8A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 4).
RC   TISSUE=Brain, and Fetal brain;
RX   MEDLINE=97442476; PubMed=9295353;
RA   Plummer N.W., McBurney M.W., Meisler M.H.;
RT   "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT   two-domain protein in fetal brain and non-neuronal cells.";
RL   J. Biol. Chem. 272:24008-24015(1997).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX   MEDLINE=99047535; PubMed=9828131;
RA   Plummer N.W., Galt J., Jones J.M., Burgess D.L., Sprunger L.K.,
RA   Kohrman D.C., Meisler M.H.;
RT   "Exon organization, coding sequence, physical mapping, and polymorphic
RT   intragenic markers for the human neuronal sodium channel gene SCN8A.";
RL   Genomics 54:287-296(1998).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Lin C., Numakura C., Kiyoshi H.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Jeong S.-Y., Goto J., Kanazawa I.;
RT   "Cloning of cDNA for human voltage-gated sodium channel alpha subunit,
RT   SCN8A.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
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CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1;
CC         IsoId=Q9UQD0-1; Sequence=Displayed;
CC       Name=2; Synonyms=5A;
CC         IsoId=Q9UQD0-2; Sequence=VSP_050589, VSP_050590;
CC       Name=3;
CC         IsoId=Q9UQD0-3; Sequence=VSP_050591;
CC       Name=4; Synonyms=18N;
CC         IsoId=Q9UQD0-4; Sequence=VSP_050592, VSP_050593;
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF050736; AAD15789.1; -.
DR   EMBL; AF050711; AAD15789.1; JOINED.
DR   EMBL; AF050712; AAD15789.1; JOINED.
DR   EMBL; AF050713; AAD15789.1; JOINED.
DR   EMBL; AF050714; AAD15789.1; JOINED.
DR   EMBL; AF050715; AAD15789.1; JOINED.
DR   EMBL; AF050716; AAD15789.1; JOINED.
DR   EMBL; AF050717; AAD15789.1; JOINED.
DR   EMBL; AF050718; AAD15789.1; JOINED.
DR   EMBL; AF050719; AAD15789.1; JOINED.
DR   EMBL; AF050720; AAD15789.1; JOINED.
DR   EMBL; AF050721; AAD15789.1; JOINED.
DR   EMBL; AF050722; AAD15789.1; JOINED.
DR   EMBL; AF050723; AAD15789.1; JOINED.
DR   EMBL; AF050724; AAD15789.1; JOINED.
DR   EMBL; AF050725; AAD15789.1; JOINED.
DR   EMBL; AF050726; AAD15789.1; JOINED.
DR   EMBL; AF050727; AAD15789.1; JOINED.
DR   EMBL; AF050728; AAD15789.1; JOINED.
DR   EMBL; AF050729; AAD15789.1; JOINED.
DR   EMBL; AF050730; AAD15789.1; JOINED.
DR   EMBL; AF050731; AAD15789.1; JOINED.
DR   EMBL; AF050732; AAD15789.1; JOINED.
DR   EMBL; AF050733; AAD15789.1; JOINED.
DR   EMBL; AF050734; AAD15789.1; JOINED.
DR   EMBL; AF050735; AAD15789.1; JOINED.
DR   EMBL; AF049618; AAD20439.1; -.
DR   EMBL; AB027567; BAA78033.1; -.
DR   EMBL; AF225988; AAF35390.1; -.
DR   HSSP; P04775; 1BYY.
DR   Genew; HGNC:10596; SCN8A.
DR   MIM; 600702; -.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IC.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; NAS.
DR   GO; GO:0006814; P:sodium ion transport; NAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008054; Na_channel8.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01667; NACHANNEL8.
DR   PROSITE; PS50096; IQ; 1.
KW   Alternative splicing; ATP-binding; Glycoprotein; Ion transport;
KW   Ionic channel; Multigene family; Repeat; Sodium channel;
KW   Transmembrane; Voltage-gated channel.
FT   REPEAT      114    442       I.
FT   REPEAT      735   1007       II.
FT   REPEAT     1180   1495       III.
FT   REPEAT     1504   1801       IV.
FT   TRANSMEM    128    151       S1 of repeat I.
FT   TRANSMEM    160    179       S2 of repeat I.
FT   TRANSMEM    193    211       S3 of repeat I.
FT   TRANSMEM    218    237       S4 of repeat I.
FT   TRANSMEM    253    277       S5 of repeat I.
FT   TRANSMEM    388    413       S6 of repeat I.
FT   TRANSMEM    748    772       S1 of repeat II.
FT   TRANSMEM    784    807       S2 of repeat II.
FT   TRANSMEM    816    835       S3 of repeat II.
FT   TRANSMEM    842    862       S4 of repeat II.
FT   TRANSMEM    878    898       S5 of repeat II.
FT   TRANSMEM    952    977       S6 of repeat II.
FT   TRANSMEM   1194   1217       S1 of repeat III.
FT   TRANSMEM   1231   1256       S2 of repeat III.
FT   TRANSMEM   1263   1284       S3 of repeat III.
FT   TRANSMEM   1289   1310       S4 of repeat III.
FT   TRANSMEM   1330   1351       S5 of repeat III.
FT   TRANSMEM   1438   1464       S6 of repeat III.
FT   TRANSMEM   1518   1541       S1 of repeat IV.
FT   TRANSMEM   1553   1576       S2 of repeat IV.
FT   TRANSMEM   1583   1606       S3 of repeat IV.
FT   TRANSMEM   1617   1638       S4 of repeat IV.
FT   TRANSMEM   1654   1676       S5 of repeat IV.
FT   TRANSMEM   1742   1766       S6 of repeat IV.
FT   DOMAIN     1895   1924       IQ.
FT   NP_BIND     893    900       ATP (Potential).
FT   CARBOHYD    215    215       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    289    289       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    295    295       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    326    326       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    544    544       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    640    640       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    877    877       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1047   1047       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1064   1064       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1091   1091       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1358   1358       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1372   1372       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1383   1383       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1768   1768       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    207    207       I -> V (in isoform 2).
FT                                 /FTId=VSP_050589.
FT   VARSPLIC    212    212       N -> D (in isoform 2).
FT                                 /FTId=VSP_050590.
FT   VARSPLIC    666    666       E -> EVKIDKAATDDS (in isoform 3).
FT                                 /FTId=VSP_050591.
FT   VARSPLIC   1275   1283       SLVSLIANA -> PLNLSGLI (in isoform 4).
FT                                 /FTId=VSP_050592.
FT   VARSPLIC   1284   1980       Missing (in isoform 4).
FT                                 /FTId=VSP_050593.
FT   CONFLICT      5      5       L -> V (in Ref. 4).
FT   CONFLICT    133    133       V -> L (in Ref. 1).
FT   CONFLICT    257    257       L -> M (in Ref. 4).
FT   CONFLICT    274    278       MGNLR -> HGEPS (in Ref. 4).
FT   CONFLICT    453    453       T -> N (in Ref. 4).
FT   CONFLICT    477    477       S -> F (in Ref. 4).
FT   CONFLICT    483    483       L -> I (in Ref. 4).
FT   CONFLICT    492    492       R -> S (in Ref. 4).
FT   CONFLICT    504    504       S -> F (in Ref. 4).
FT   CONFLICT    547    548       LL -> MF (in Ref. 4).
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FT   CONFLICT   1445   1445       V -> I (in Ref. 1).
FT   CONFLICT   1519   1519       V -> I (in Ref. 1).
FT   CONFLICT   1702   1702       T -> A (in Ref. 4).
SQ   SEQUENCE   1980 AA;  225279 MW;  0EFC7BFB137FD4F0 CRC64;

  Query Match             89.3%;  Score 25;  DB 1;  Length 1980;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-14;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||||
Db        956 VFMMVMVIGNLVVLNLFLALLLSSF 980


RESULT 19
O88421
ID   O88421      PRELIMINARY;      PRT;  1988 AA.
AC   O88421;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel variant rPN4a.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dorsal root ganglia;
RX   MEDLINE=98264329; PubMed=9603190;
RA   Dietrich P.S., McGivern J.G., Delgado S.G., Koch B.D., Eglen R.M.,
RA   Hunter J.C., Sangameswaran L.;
RT   "Functional analysis of a voltage-gated sodium channel and its splice
RT   variant from rat dorsal root ganglia.";
RL   J. Neurochem. 70:2262-2272(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AF049240; AAC26015.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR000183; Decarbxylse2.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008054; Na_channel8.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01667; NACHANNEL8.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
DR   PROSITE; PS00878; ODR_DC_2_1; UNKNOWN_1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1988 AA;  226186 MW;  C1F7D87FDC266C8F CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 1988;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-14;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||||
Db        964 VFMMVMVIGNLVVLNLFLALLLSSF 988


RESULT 20
Q15858
ID   Q15858      PRELIMINARY;      PRT;  1977 AA.
AC   Q15858;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel alpha subunit.
GN   Name=hNE-Na;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thyroid;
RX   MEDLINE=95237189; PubMed=7720699;
RA   Klugbauer N., Lacinova L., Flockerzi V., Hofmann F.;
RT   "Structure and functional expression of a new member of the
RT   tetrodotoxin-sensitive voltage-activated sodium channel family from
RT   human neuroendocrine cells.";
RL   EMBO J. 14:1084-1090(1995).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; X82835; CAA58042.1; -.
DR   PIR; S54771; S54771.
DR   HSSP; P04775; 1BYY.
DR   Genew; HGNC:10597; SCN9A.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; TAS.
DR   GO; GO:0006814; P:sodium ion transport; TAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1977 AA;  225195 MW;  17D67CBC32BC15FB CRC64;

  Query Match             82.1%;  Score 23;  DB 2;  Length 1977;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-12;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        938 MMVMVIGNLVVLNLFLALLLSSF 960


RESULT 21
Q28644
ID   Q28644      PRELIMINARY;      PRT;  1984 AA.
AC   Q28644;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel alpha-subunit.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=New Zealand White; TISSUE=Sciatic nerve;
RX   MEDLINE=96074641; PubMed=7479931;
```

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RA   Belcher S.M., Zerillo C.A., Levenson R., Ritchie J.M., Howe J.R.;
RT   "Cloning of a sodium channel alpha subunit from rabbit Schwann
RT   cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:11034-11038(1995).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; U35238; AAA89159.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1984 AA;  225748 MW;  98F76860C9866AA0 CRC64;

  Query Match             82.1%;  Score 23;  DB 2;  Length 1984;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-12;
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Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
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Db        946 MMVMVIGNLVVLNLFLALLLSSF 968


RESULT 22
O08562
ID   O08562      PRELIMINARY;      PRT;  1984 AA.
AC   O08562;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   PN1 (Voltage-gated sodium channel) (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97188502; PubMed=9037087;
RA   Toledo-Aral J.J., Moss B.L., He Z.J., Koszowski A.G., Whisenand T.,
RA   Levinson S.R., Wolf J.J., Silos-Santiago I., Halegoua S., Mandel G.;
RT   "Identification of PN1, a predominant voltage-dependent sodium channel
RT   expressed principally in peripheral neurons.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:1527-1532(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97007982; PubMed=8854872;
RA   Kozak C.A., Sangameswaran L.;
RT   "Genetic mapping of the peripheral sodium channel genes, Scn9a and
RT   Scn10a, in the mouse.";
RL   Mamm. Genome 7:787-788(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Sangameswaran L., Fish L.M., Koch B.D., Rabert D.K., Delgado S.G.,
RA   Ilnicka M., Jakeman L.B., Novakovic S., Wong K., Sze P., Tzoumaka E.,
RA   Stewart G.R., Herman R.C., Chan H., Eglen R.M., Hunter J.C.;
RT   "A novel tetrodotoxin-sensitive, voltage-gated sodium channel
RT   expressed in rat and human dorsal root ganglia.";
RL   J. Biol. Chem. 0:0-0(1997).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; U79568; AAB50403.1; -.
DR   EMBL; AF000368; AAB80701.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
FT   NON_TER    1984   1984
SQ   SEQUENCE   1984 AA;  226037 MW;  386C38B9B5097091 CRC64;

  Query Match             82.1%;  Score 23;  DB 2;  Length 1984;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-12;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        948 MMVMVIGNLVVLNLFLALLLSSF 970


RESULT 23
Q800T9
ID   Q800T9      PRELIMINARY;      PRT;   473 AA.
AC   Q800T9;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel 6 (Fragment).
OS   Ictalurus punctatus (Channel catfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC   Ictaluridae; Ictalurus.
OX   NCBI_TaxID=7998;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lu Y., Lopreato G.F., Zakon H.H.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY204537; AAO60425.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER      1      1
FT   NON_TER    473    473
SQ   SEQUENCE   473 AA;  53617 MW;  D922504FD1C0DF1B CRC64;

  Query Match             78.6%;  Score 22;  DB 2;  Length 473;
  Best Local Similarity   100.0%;  Pred. No. 3e-12;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          7 MVMVIGNLVVLNLFLALLLSSF 28
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Db         12 MVMVIGNLVVLNLFLALLLSSF 33


RESULT 24
Q800U1
ID   Q800U1      PRELIMINARY;      PRT;   488 AA.
AC   Q800U1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel 4 (Fragment).
OS   Ictalurus punctatus (Channel catfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC   Ictaluridae; Ictalurus.
OX   NCBI_TaxID=7998;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lu Y., Lopreato G.F., Zakon H.H.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY204535; AAO60423.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1      1
FT   NON_TER     488    488
SQ   SEQUENCE   488 AA;  55100 MW;  379A1BAA105F3A8F CRC64;

  Query Match             78.6%;  Score 22;  DB 2;  Length 488;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-12;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 MVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db         12 MVMVIGNLVVLNLFLALLLSSF 33


RESULT 25
Q90Z27
ID   Q90Z27      PRELIMINARY;      PRT;   744 AA.
AC   Q90Z27;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel 4 (Fragment).
OS   Sternopygus macrurus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC   Sternopygidae; Sternopygus.
OX   NCBI_TaxID=77841;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21310016; PubMed=11416226;
RA   Lopreato G.F., Lu Y., Southwell A., Atkinson N.S., Hillis D.M.,
RA   Wilcox T.P., Zakon H.H.;
RT   "Evolution and divergence of sodium channel genes in vertebrates.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7588-7592(2001).
DR   EMBL; AF378142; AAK55440.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 2.
DR   Pfam; PF06512; Na_trans_assoc; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1      1
FT   NON_TER     744    744
SQ   SEQUENCE   744 AA;  84557 MW;  B0D6E7B203893C28 CRC64;

  Query Match             78.6%;  Score 22;  DB 2;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 MVMVIGNLVVLNLFLALLLSSF 28
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Db        184 MVMVIGNLVVLNLFLALLLSSF 205


Search completed: January 27, 2005, 17:51:32
Job time : 94.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:36:50 ; Search time 22.5 Seconds
(without alignments)
82.529 Million cell updates/sec

Title: US-10-608-584-13
Perfect score: 28
Sequence: 1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28

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Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

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Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	100.0	2005	3	US-08-836-325-7	Sequence 7, Appli
2	28	100.0	2005	4	US-09-457-571-7	Sequence 7, Appli
3	25	89.3	1976	3	US-09-024-020B-9	Sequence 9, Appli
4	25	89.3	1976	3	US-09-425-043-9	Sequence 9, Appli
5	25	89.3	1978	3	US-09-024-020B-3	Sequence 3, Appli
6	25	89.3	1978	3	US-09-425-043-3	Sequence 3, Appli
7	25	89.3	1988	3	US-09-024-020B-4	Sequence 4, Appli
8	25	89.3	1988	3	US-09-425-043-4	Sequence 4, Appli
9	23	82.1	1835	3	US-08-836-325-15	Sequence 15, Appl
10	23	82.1	1835	4	US-09-457-571-15	Sequence 15, Appl
11	23	82.1	1969	3	US-08-836-325-16	Sequence 16, Appl
12	23	82.1	1969	4	US-09-457-571-16	Sequence 16, Appl
13	23	82.1	1977	4	US-09-976-594-757	Sequence 757, App
14	23	82.1	1977	4	US-09-919-039-367	Sequence 367, App
15	23	82.1	1984	3	US-08-836-325-10	Sequence 10, Appl
16	23	82.1	1984	4	US-09-457-571-10	Sequence 10, Appl
17	23	82.1	1989	3	US-08-836-325-11	Sequence 11, Appl
18	23	82.1	1989	3	US-08-836-325-12	Sequence 12, Appl
19	23	82.1	1989	4	US-09-457-571-11	Sequence 11, Appl
20	23	82.1	1989	4	US-09-457-571-12	Sequence 12, Appl
21	22	78.6	1836	4	US-10-162-012-24	Sequence 24, Appl
22	21	75.0	1024	4	US-09-562-737-81	Sequence 81, Appl
23	21	75.0	2016	3	US-09-634-920-4	Sequence 4, Appli
24	21	75.0	2016	4	US-09-514-907A-2	Sequence 2, Appli
25	21	75.0	2016	4	US-09-896-994-2	Sequence 2, Appli
26	21	75.0	2016	4	US-09-840-125-4	Sequence 4, Appli
27	17	60.7	1820	3	US-07-998-289B-8	Sequence 8, Appli
28	17	60.7	2100	2	US-08-808-793-23	Sequence 23, Appl
29	17	60.7	2100	3	US-08-772-512A-19	Sequence 19, Appl
30	17	60.7	2105	2	US-08-808-793-3	Sequence 3, Appli
31	17	60.7	2105	3	US-08-772-512A-3	Sequence 3, Appli
32	16	57.1	813	3	US-08-836-325-8	Sequence 8, Appli
33	16	57.1	813	4	US-09-457-571-8	Sequence 8, Appli
34	16	57.1	1011	3	US-08-836-325-2	Sequence 2, Appli
35	16	57.1	1011	4	US-09-457-571-2	Sequence 2, Appli
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37	12	42.9	2104	3	US-08-772-512A-4	Sequence 4, Appli
38	9	32.1	1024	4	US-09-562-737-82	Sequence 82, Appl
39	9	32.1	1024	4	US-09-562-737-83	Sequence 83, Appl
40	9	32.1	1024	4	US-09-562-737-84	Sequence 84, Appl
41	9	32.1	1024	4	US-09-562-737-85	Sequence 85, Appl
42	9	32.1	1024	4	US-09-562-737-86	Sequence 86, Appl
43	9	32.1	1024	4	US-09-562-737-87	Sequence 87, Appl
44	9	32.1	1024	4	US-09-562-737-88	Sequence 88, Appl
45	9	32.1	1024	4	US-09-562-737-89	Sequence 89, Appl
46	9	32.1	1024	4	US-09-562-737-90	Sequence 90, Appl
47	9	32.1	1956	3	US-08-843-417-2	Sequence 2, Appli
48	9	32.1	1956	3	US-08-843-417-10	Sequence 10, Appl
49	9	32.1	1956	4	US-09-527-013-2	Sequence 2, Appli
50	9	32.1	1956	4	US-09-527-013-10	Sequence 10, Appl
51	9	32.1	1957	4	US-08-669-656A-2	Sequence 2, Appli
52	9	32.1	1957	4	US-08-669-656A-8	Sequence 8, Appli
53	9	32.1	2132	4	US-08-669-656A-6	Sequence 6, Appli
54	8	28.6	501	1	US-08-331-394-4	Sequence 4, Appli
55	8	28.6	501	1	US-08-250-858-4	Sequence 4, Appli
56	8	28.6	501	1	US-08-446-915-4	Sequence 4, Appli
57	8	28.6	501	2	US-08-744-139-4	Sequence 4, Appli
58	8	28.6	501	4	US-08-779-599-4	Sequence 4, Appli
59	8	28.6	501	5	PCT-US95-06639-4	Sequence 4, Appli
60	7	25.0	104	6	5187075-5	Patent No. 5187075
61	7	25.0	197	3	US-08-833-488B-4	Sequence 4, Appli
62	7	25.0	197	3	US-08-833-488B-9	Sequence 9, Appli
63	7	25.0	197	3	US-08-833-488B-28	Sequence 28, Appl
64	7	25.0	199	3	US-08-833-488B-14	Sequence 14, Appl
65	7	25.0	204	6	5187075-6	Patent No. 5187075
66	7	25.0	253	3	US-08-833-488B-20	Sequence 20, Appl
67	7	25.0	431	4	US-09-592-998C-9	Sequence 9, Appli
68	7	25.0	435	4	US-09-592-998C-10	Sequence 10, Appl
69	7	25.0	451	4	US-09-446-861-127	Sequence 127, App
70	7	25.0	461	3	US-09-122-210-2	Sequence 2, Appli
71	7	25.0	461	3	US-09-443-681-2	Sequence 2, Appli
72	7	25.0	573	4	US-09-643-657-18	Sequence 18, Appl
73	7	25.0	586	4	US-10-140-002-46	Sequence 46, Appl
74	7	25.0	591	4	US-09-643-657-3	Sequence 3, Appli
75	7	25.0	633	2	US-08-736-770-3	Sequence 3, Appli
76	7	25.0	728	4	US-09-252-991A-23738	Sequence 23738, A
77	7	25.0	1023	4	US-10-140-002-200	Sequence 200, App
78	7	25.0	1233	4	US-09-354-147C-7	Sequence 7, Appli
79	7	25.0	1243	4	US-09-354-147C-8	Sequence 8, Appli
80	7	25.0	1498	2	US-08-404-531B-28	Sequence 28, Appl
81	7	25.0	1498	2	US-08-404-531B-29	Sequence 29, Appl
82	7	25.0	1498	3	US-08-476-900A-28	Sequence 28, Appl
83	7	25.0	1498	3	US-08-476-900A-29	Sequence 29, Appl
84	7	25.0	1498	3	US-08-488-546A-28	Sequence 28, Appl
85	7	25.0	1498	3	US-08-488-546A-29	Sequence 29, Appl
86	7	25.0	1580	3	US-08-726-320-1	Sequence 1, Appli
87	7	25.0	1580	3	US-09-208-716-1	Sequence 1, Appli
88	7	25.0	1581	2	US-08-404-531B-6	Sequence 6, Appli
89	7	25.0	1581	3	US-08-476-900A-6	Sequence 6, Appli
90	7	25.0	1581	3	US-08-488-546A-6	Sequence 6, Appli
91	7	25.0	1581	3	US-08-726-320-3	Sequence 3, Appli
92	7	25.0	1581	3	US-08-726-320-4	Sequence 4, Appli
93	7	25.0	1581	3	US-09-208-716-3	Sequence 3, Appli
94	7	25.0	1581	3	US-09-208-716-4	Sequence 4, Appli
95	7	25.0	1582	2	US-08-404-531B-9	Sequence 9, Appli
96	7	25.0	1582	3	US-08-476-900A-9	Sequence 9, Appli
97	7	25.0	1582	3	US-08-488-546A-9	Sequence 9, Appli
98	7	25.0	1582	3	US-08-726-320-5	Sequence 5, Appli
99	7	25.0	1582	3	US-09-208-716-5	Sequence 5, Appli
100	7	25.0	1765	4	US-09-354-147C-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-08-836-325-7
; Sequence 7, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2005 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-836-325-7

  Query Match             100.0%;  Score 28;  DB 3;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
              ||||||||||||||||||||||||||||
Db        959 CLTVFMMVMVIGNLVVLNLFLALLLSSF 986


RESULT 2
US-09-457-571-7
; Sequence 7, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2005 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-457-571-7

  Query Match             100.0%;  Score 28;  DB 4;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-18;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CLTVFMMVMVIGNLVVLNLFLALLLSSF 28
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Db        959 CLTVFMMVMVIGNLVVLNLFLALLLSSF 986


RESULT 3
US-09-024-020B-9
; Sequence 9, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
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;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1976 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-024-020B-9

  Query Match             89.3%;  Score 25;  DB 3;  Length 1976;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-16;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
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Db        952 VFMMVMVIGNLVVLNLFLALLLSSF 976


RESULT 4
US-09-425-043-9
; Sequence 9, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1976 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-425-043-9

  Query Match             89.3%;  Score 25;  DB 3;  Length 1976;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-16;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||||
Db        952 VFMMVMVIGNLVVLNLFLALLLSSF 976


RESULT 5
US-09-024-020B-3
; Sequence 3, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  1978 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-024-020B-3

  Query Match             89.3%;  Score 25;  DB 3;  Length 1978;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-16;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
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Db        954 VFMMVMVIGNLVVLNLFLALLLSSF 978


RESULT 6
US-09-425-043-3
; Sequence 3, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1978 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-425-043-3

  Query Match             89.3%;  Score 25;  DB 3;  Length 1978;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-16;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
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Db        954 VFMMVMVIGNLVVLNLFLALLLSSF 978


RESULT 7
US-09-024-020B-4
; Sequence 4, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1988 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-024-020B-4

  Query Match             89.3%;  Score 25;  DB 3;  Length 1988;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-16;
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Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
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Db        964 VFMMVMVIGNLVVLNLFLALLLSSF 988


RESULT 8
US-09-425-043-4
; Sequence 4, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
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;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1988 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-425-043-4

  Query Match             89.3%;  Score 25;  DB 3;  Length 1988;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-16;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VFMMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||||
Db        964 VFMMVMVIGNLVVLNLFLALLLSSF 988


RESULT 9
US-08-836-325-15
; Sequence 15, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1835 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-836-325-15

  Query Match             82.1%;  Score 23;  DB 3;  Length 1835;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-14;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        882 MMVMVIGNLVVLNLFLALLLSSF 904


RESULT 10
US-09-457-571-15
; Sequence 15, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
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;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1835 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-09-457-571-15

  Query Match             82.1%;  Score 23;  DB 4;  Length 1835;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-14;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        882 MMVMVIGNLVVLNLFLALLLSSF 904


RESULT 11
US-08-836-325-16
; Sequence 16, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1969 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-836-325-16

  Query Match             82.1%;  Score 23;  DB 3;  Length 1969;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-14;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        938 MMVMVIGNLVVLNLFLALLLSSF 960


RESULT 12
US-09-457-571-16
; Sequence 16, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1969 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-457-571-16

  Query Match             82.1%;  Score 23;  DB 4;  Length 1969;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-14;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        938 MMVMVIGNLVVLNLFLALLLSSF 960


RESULT 13
US-09-976-594-757
; Sequence 757, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 757
;   LENGTH: 1977
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 1719478CD1
US-09-976-594-757

  Query Match             82.1%;  Score 23;  DB 4;  Length 1977;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-14;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        938 MMVMVIGNLVVLNLFLALLLSSF 960


RESULT 14
US-09-919-039-367
; Sequence 367, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
;  APPLICANT: Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;  FILE REFERENCE: PA-0035 US
;  CURRENT APPLICATION NUMBER: US/09/919,039
;  CURRENT FILING DATE:  2002-09-09
;  PRIOR APPLICATION NUMBER: 60/222,113
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 401
;  SOFTWARE: PERL Program
; SEQ ID NO 367
;   LENGTH: 1977
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6727066 1719478CD1
US-09-919-039-367

  Query Match             82.1%;  Score 23;  DB 4;  Length 1977;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-14;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        938 MMVMVIGNLVVLNLFLALLLSSF 960


RESULT 15
US-08-836-325-10
; Sequence 10, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1984 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-836-325-10

  Query Match             82.1%;  Score 23;  DB 3;  Length 1984;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-14;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        948 MMVMVIGNLVVLNLFLALLLSSF 970


RESULT 16
US-09-457-571-10
; Sequence 10, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
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;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1984 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-457-571-10

  Query Match             82.1%;  Score 23;  DB 4;  Length 1984;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-14;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        948 MMVMVIGNLVVLNLFLALLLSSF 970


RESULT 17
US-08-836-325-11
; Sequence 11, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1989 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-836-325-11

  Query Match             82.1%;  Score 23;  DB 3;  Length 1989;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-14;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||||
Db        949 MMVMVIGNLVVLNLFLALLLSSF 971


RESULT 18
US-08-836-325-12
; Sequence 12, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
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```
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/836,325
;       FILING DATE:  2-MAY-1997
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/14251
;       FILING DATE:  02-NOV-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/482,401
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/334,029
;       FILING DATE:  02-NOV-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ludwig, Steven R.
;       REGISTRATION NUMBER:  36,203
;       REFERENCE/DOCKET NUMBER:  0917.0240002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1989 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  protein
US-08-836-325-12

  Query Match             82.1%;  Score 23;  DB 3;  Length 1989;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-14;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
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Db        949 MMVMVIGNLVVLNLFLALLLSSF 971


RESULT 19
US-09-457-571-11
; Sequence 11, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1989 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-09-457-571-11

  Query Match             82.1%;  Score 23;  DB 4;  Length 1989;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-14;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
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Db        949 MMVMVIGNLVVLNLFLALLLSSF 971


RESULT 20
US-09-457-571-12
; Sequence 12, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
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  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  08/334,029
    FILING DATE:  02-NOV-1994
  ATTORNEY/AGENT INFORMATION:
    NAME:  Ludwig, Steven R.
    REGISTRATION NUMBER:  36,203
    REFERENCE/DOCKET NUMBER:  0917.0240003
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  202-371-2600
    TELEFAX:  202-371-2540
  INFORMATION FOR SEQ ID NO:  12:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  1989 amino acids
      TYPE:  amino acid
      STRANDEDNESS:  not relevant
      TOPOLOGY:  not relevant
    MOLECULE TYPE:  protein
US-09-457-571-12

  Query Match           82.1%;  Score 23;  DB 4;  Length 1989;
  Best Local Similarity  100.0%;  Pred. No. 7.2e-14;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 MMVMVIGNLVVLNLFLALLLSSF 28
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Db        949 MMVMVIGNLVVLNLFLALLLSSF 971


RESULT 21
US-10-162-012-24
; Sequence 24, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  Gu, Wei
;  TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
;  FILE REFERENCE: 10448-190001
;  CURRENT APPLICATION NUMBER: US/10/162,012
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: US 60/209,845
;  PRIOR FILING DATE: 2000-06-06
;  PRIOR APPLICATION NUMBER: US 09/875,321
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: PCT/US01/18340
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/209,257
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,423
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18398
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/209,238
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,363
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18247
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/227,068
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: US 09/928,530
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: PCT/US01/25475
;  PRIOR FILING DATE: 2001-08-15
;  PRIOR APPLICATION NUMBER: US 60/226,770
;  PRIOR FILING DATE: 2000-08-21
;  PRIOR APPLICATION NUMBER: US 09/934,421
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: PCT/US01/26096
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: US 60/279,281
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 10/109,029
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: PCT/US02/09728
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 60/290,288
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US (not assigned)
;  PRIOR FILING DATE: 2002-05-13
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 1836
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-162-012-24

  Query Match           78.6%;  Score 22;  DB 4;  Length 1836;
  Best Local Similarity  100.0%;  Pred. No. 6.1e-13;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 MVMVIGNLVVLNLFLALLLSSF 28
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Db        784 MVMVIGNLVVLNLFLALLLSSF 805


RESULT 22
US-09-562-737-81
; Sequence 81, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
;  APPLICANT:  Herz, Joachim
;  APPLICANT:  Gotthardt, Michael
;  TITLE OF INVENTION:  LDL Receptor Signaling Pathways
;  FILE REFERENCE:  UTSW0708
;  CURRENT APPLICATION NUMBER: US/09/562,737
;  CURRENT FILING DATE:  2000-05-01
;  NUMBER OF SEQ ID NOS:  132
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 1024
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Sequence
US-09-562-737-81

  Query Match           75.0%;  Score 21;  DB 4;  Length 1024;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VMVIGNLVVLNLFLALLLSSF 28
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Db        918 VMVIGNLVVLNLFLALLLSSF 938


RESULT 23
US-09-634-920-4
; Sequence 4, Application US/09634920
; Patent No. 6342357
; GENERAL INFORMATION:
;  APPLICANT:  Splawski, Igor
;  APPLICANT:  Keating, Mark T.
;  TITLE OF INVENTION:  ALTERATIONS IN THE LONG QT SYNDROM
;  TITLE OF INVENTION:  SCN5A AND METHODS FOR DETECTING
;  FILE REFERENCE:  2323-155
;  CURRENT APPLICATION NUMBER: US/09/634,920
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/190,057
;  PRIOR FILING DATE:  2000-03-17
;  PRIOR APPLICATION NUMBER:  60/147,48
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PatentIn Ver. 2.
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; SEQ ID NO 4
;   LENGTH: 2016
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-634-920-4

  Query Match             75.0%;  Score 21;  DB 3;  Length 2016;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||
Db        922 VMVIGNLVVLNLFLALLLSSF 942


RESULT 24
US-09-514-907A-2
; Sequence 2, Application US/09514907A
; Patent No. 6567705
;   GENERAL INFORMATION:
;        APPLICANT: Kenneth B. Stokes
;                   Jos,e Morissette
;        TITLE OF INVENTION: SYSTEMS FOR ENHANCING CARDIAC SIGNAL
;                            SENSING BY CARDIAC PACEMAKERS THROUGH
;                            GENETIC TREATMENT
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6567705ris LLP
;             STREET: One Liberty Place - 46th Floor
;             CITY: Philadelphia
;             STATE: PA
;             COUNTRY: U.S.A.
;             ZIP: 19103
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WordPerfect 6.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/514,907A
;             FILING DATE: 08-Feb-2000
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Paul K. Legaard
;             REGISTRATION NUMBER: 38,534
;             REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (215) 568-3100
;             TELEFAX: (215) 568-3439
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2016 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: unknown
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-514-907A-2

  Query Match             75.0%;  Score 21;  DB 4;  Length 2016;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VMVIGNLVVLNLFLALLLSSF 28
              |||||||||||||||||||||
Db        922 VMVIGNLVVLNLFLALLLSSF 942


RESULT 25
US-09-896-994-2
; Sequence 2, Application US/09896994
; Patent No. 6665563
;   GENERAL INFORMATION:
;        APPLICANT: Ken Stokes
;                   Jos e Morissette
;        TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC
;                            SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATME
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6665563ris
;             STREET: One Liberty Place - 46th Floor
;             CITY: Philadelphia
;             STATE: PA
;             COUNTRY: U.S.A.
;             ZIP: 19103
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WordPerfect 6.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/896,994
;             FILING DATE: 02-Jul-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/514,907
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Paul K. Legaard
;             REGISTRATION NUMBER: 38,534
;             REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (215) 568-3100
;             TELEFAX: (215) 568-3439
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2016 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: unknown
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-896-994-2

  Query Match             75.0%;  Score 21;  DB 4;  Length 2016;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VMVIGNLVVLNLFLALLLSSF 28
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Db        922 VMVIGNLVVLNLFLALLLSSF 942


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Job time : 23.5 secs
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GenCore version 5.1.6

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(without alignments)
116.120 Million cell updates/sec

Title: US-10-608-584-19
Perfect score: 28
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Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

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5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	28	100.0	1836	7	ADE59630	Ade59630 Human Pro
5	28	100.0	1836	7	ADE63029	Ade63029 Human Pro
6	28	100.0	1836	8	ADQ17412	Adq17412 Human sof
7	28	100.0	1855	7	ADB78597	Adb78597 Human sod
8	28	100.0	1950	7	ADB78607	Adb78607 Human sod
9	28	100.0	1951	4	AAB99678	Aab99678 Human adu
10	28	100.0	1951	4	AAB99679	Aab99679 Human neo
11	28	100.0	1951	7	ADE59628	Ade59628 Rat Prote
12	28	100.0	1951	8	ADL06576	Adl06576 Human tum
13	28	100.0	1962	5	AAE20511	Aae20511 Human ion
14	28	100.0	1973	5	AAE20516	Aae20516 Human ion
15	28	100.0	1981	7	ABR83185	Abr83185 Human SCN
16	28	100.0	1998	5	AAE20510	Aae20510 Human ion
17	28	100.0	1998	7	ABR83184	Abr83184 Human SCN
18	28	100.0	1999	5	ABB06026	Abb06026 Human sod
19	28	100.0	2000	5	ABB06027	Abb06027 Human sod
20	28	100.0	2000	8	ADK81762	Adk81762 Human Nav
21	28	100.0	2005	4	AAB99676	Aab99676 Human adu
22	28	100.0	2005	4	AAB99677	Aab99677 Human neo
23	28	100.0	2005	5	ABB83627	Abb83627 Human GEF
24	28	100.0	2005	7	ADB78604	Adb78604 Human sod
25	28	100.0	2005	7	ADB78603	Adb78603 Human sod
26	28	100.0	2005	7	ADB78605	Adb78605 Human sod
27	28	100.0	2005	7	ADC46947	Adc46947 Human SCN
28	28	100.0	2009	4	AAB99674	Aab99674 Human adu
29	28	100.0	2009	5	AAE20515	Aae20515 Human ion
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34	28	100.0	2009	5	ABG69290	Abg69290 Human sod
35	28	100.0	2009	5	ABB83626	Abb83626 Human GEF
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37	28	100.0	2009	7	ADB78599	Adb78599 Human sod
38	28	100.0	2009	7	ADB78595	Adb78595 Human sod
39	28	100.0	2009	7	ADB78593	Adb78593 Human sod
40	28	100.0	2009	7	ADB78594	Adb78594 Human sod
41	28	100.0	2009	7	ADB78598	Adb78598 Human sod
42	28	100.0	2009	7	ABR83180	Abr83180 Human SCN
43	28	100.0	2009	7	ADE57563	Ade57563 Human Pro
44	28	100.0	2009	7	ADE57561	Ade57561 Rat Prote
45	25	89.3	1011	2	AAR99638	Aar99638 Periphera
46	25	89.3	1976	7	ADE57386	Ade57386 Rat Prote
47	25	89.3	1978	2	AAW69361	Aaw69361 Tetrodoto
48	25	89.3	1980	3	AAB23563	Aab23563 Human sod
49	25	89.3	1980	5	AAO14927	Aao14927 Human sod
50	25	89.3	1980	7	ADB78600	Adb78600 Human sod
51	25	89.3	1980	7	ADB78606	Adb78606 Human sod
52	25	89.3	1984	2	AAR99639	Aar99639 Periphera
53	25	89.3	1984	7	ADE54547	Ade54547 Rat Prote
54	25	89.3	1984	7	ADE54551	Ade54551 Rat Prote
55	25	89.3	1984	7	ADE63027	Ade63027 Rat Prote
56	25	89.3	1988	2	AAW69362	Aaw69362 Tetrodoto
57	25	89.3	1989	2	AAR92317	Aar92317 Periphera
58	25	89.3	2015	4	AAB82242	Aab82242 Human SCN
59	25	89.3	2015	7	ADF56441	Adf56441 Human Nav
60	25	89.3	2015	8	ADM34001	Adm34001 Human SCN
61	25	89.3	2015	8	ADM33999	Adm33999 Human SCN
62	25	89.3	2016	2	AAW23994	Aaw23994 Human hH1
63	25	89.3	2016	4	AAB82239	Aab82239 Human SCN
64	25	89.3	2016	4	AAB82240	Aab82240 Human SCN
65	25	89.3	2016	4	AAB82245	Aab82245 Human SCN
66	25	89.3	2016	4	AAB82243	Aab82243 Human SCN
67	25	89.3	2016	4	AAB82244	Aab82244 Human SCN
68	25	89.3	2016	4	AAB82241	Aab82241 Human SCN
69	25	89.3	2016	7	ADD44756	Add44756 Human Pro
70	25	89.3	2016	7	ADE55106	Ade55106 Human Pro
71	25	89.3	2016	8	ADM33997	Adm33997 Human SCN
72	25	89.3	2016	8	ADM33995	Adm33995 Human SCN
73	21	75.0	284	2	AAY16577	Aay16577 Type 5 so
74	21	75.0	413	2	AAW89580	Aaw89580 Partial c
75	21	75.0	448	2	AAR60497	Aar60497 A non-dip
76	21	75.0	1233	4	AAB20125	Aab20125 Human sod
77	21	75.0	1243	2	AAY06598	Aay06598 Human sod
78	21	75.0	1243	4	AAB20126	Aab20126 Human sod
79	21	75.0	1444	5	AAO14926	Aao14926 Human sod
80	21	75.0	1765	2	AAY16572	Aay16572 Type 5 so
81	21	75.0	1765	2	AAY41668	Aay41668 Rat senso
82	21	75.0	1765	2	AAY06597	Aay06597 Mouse sod
83	21	75.0	1765	2	AAY06596	Aay06596 Rat sodiu
84	21	75.0	1765	4	AAB20124	Aab20124 Mouse sod
85	21	75.0	1765	4	AAB20122	Aab20122 Rat sodiu
86	21	75.0	1765	4	AAB20123	Aab20123 Rat sodiu
87	21	75.0	1765	7	ADD32192	Add32192 Rat Na v
88	21	75.0	1765	7	ADD32210	Add32210 Rat Na v
89	21	75.0	1765	7	ADD32196	Add32196 Mouse Na
90	21	75.0	1765	7	ADE55104	Ade55104 Rat Prote
91	21	75.0	1791	4	AAB20121	Aab20121 Human sod
92	21	75.0	1791	5	AAO14925	Aao14925 Human sod
93	21	75.0	1791	7	ADD32194	Add32194 Human Na
94	21	75.0	1835	2	AAR92316	Aar92316 Periphera
95	21	75.0	1977	2	AAR99641	Aar99641 Periphera
96	21	75.0	1977	8	ADE77202	Ade77202 Human pro
97	21	75.0	1977	8	ADL13028	Adl13028 Human ste
98	21	75.0	1978	7	ADE54553	Ade54553 Human Pro

99	21	75.0	1978	7	ADE54549	Ade54549 Human Pro
100	21	75.0	1989	2	AAR99640	Aar99640 Periphera

ALIGNMENTS

RESULT 1
ADF45244
ID ADF45244 standard; protein; 280 AA.
XX
AC ADF45244;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human sodium channel alpha subunit amino acid sequence.
XX
KW human; cation channel; INPIONCH05; INPIONCH06; tetrameric cation channel;
KW antiinfertility; neuroprotective; cardiovascular; immunosuppressive;
KW cerebroprotective; vasotropic; contraceptive; vaccine; infertility;
KW neurological disorder; cardiovascular disorder; autoimmune disease;
KW stroke; stroke-related disorder; pathological condition; calcium channel.
XX
OS Homo sapiens.
XX
PN WO2003099865-A1.
XX
PD 04-DEC-2003.
XX
PF 23-MAY-2003; 2003WO-GB002270.
XX
PR 24-MAY-2002; 2002GB-00012067.
XX
PA (INPH-) INPHARMATICA LTD.
XX
PI Lobley AE, Michalovich D, Allen KE, Reynolds L, Pierron VN;
XX
DR WPI; 2004-053233/05.
XX
PT New INPIONCH05 and INPIONCH06 polypeptides, useful as a contraceptive
PT agent, or for diagnosing and treating a disease or disorder, e.g.
PT infertility, neurological disorder, cardiovascular disorder, autoimmune
PT disease or stroke.
XX
PS Example 1; Fig 2; 96pp; English.
XX
CC The present invention describes cation channel polypeptides (I), termed
CC INPIONCH05 and INPIONCH06. Also described: (1) a purified nucleic acid
CC molecule (II), which: (a) encodes (I); or (b) hybridises under high
CC stringency conditions with the nucleic acid molecule of (a); (2) a vector
CC comprising (II); (3) a host cell transformed with the vector; (4) a
CC tetrameric cation channel comprising (I); (5) a ligand which binds
CC specifically to, and which preferably inhibits the activity of (I) or the
CC tetrameric cation channel; (6) a compound that either increases or
CC decreases the level of expression or activity of (I) or the tetrameric
CC cation channel; (7) a method of diagnosing a disease in a patient; (8) a
CC pharmaceutical composition comprising (I), (II), vector, host cell,
CC tetrameric cation channel, ligand, or compound; (9) a vaccine composition
CC comprising (I) or (II); (10) a method of treating a disease in a patient;
CC (11) a method of monitoring the therapeutic treatment of disease in a
CC patient; (12) a method for the identification of a compound that is
CC effective in the treatment and/or diagnosis of a disease/disorder; (13)
CC an array of nucleic acid molecules, at least one of which is (II), or one
CC or more antibodies that bind to (I) or to the tetrameric cation channel,
CC and a reagent useful for the detection of a binding reaction between the
CC antibody and (I) or tetrameric cation channel; (14) a transgenic or
CC knockout non-human animal that has been transformed to express higher,
CC lower or absent levels of (I); and (15) a method for screening for a
CC compound effective to treat a disease or disorder. (I) has
CC antiinfertility, neuroprotective, cardiovascular, immunosuppressive,
CC cerebroprotective, vasotropic and contraceptive activities, and can be
CC used in vaccines. (I), (II), vectors, tetrameric cation channels,
CC ligands, compounds, or compositions of the present invention may be used
CC as contraceptive agents, preferably a non-hormonal contraceptive agent,
CC in therapy or diagnosis of a disease or disorder, or in manufacturing a
CC medicament for the treatment of a disease or disorder, e.g. infertility,
CC neurological disorder, cardiovascular disorder, autoimmune disease,
CC stroke, stroke-related disorders or other pathological condition. (I) is
CC useful as a cation channel or a calcium channel. (I) or the tetrameric
CC cation channel is useful as a sperm-specific CatSper channel. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 280 AA;

Query Match 100.0%; Score 28; DB 8; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.4e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 246 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 273

RESULT 2
ADB78596
ID ADB78596 standard; protein; 1795 AA.
XX
AC ADB78596;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:140.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78635.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 140; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and

CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 1795 AA;

Query Match 100.0%; Score 28; DB 7; Length 1795;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1459 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1486

RESULT 3
ADE57388
ID ADE57388 standard; protein; 1836 AA.
XX
AC ADE57388;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein XP_008249, SEQ ID NO 3249.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; XP_008249.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1836 AA;

Query Match 100.0%; Score 28; DB 7; Length 1836;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1271 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1298

RESULT 4
ADE59630
ID ADE59630 standard; protein; 1836 AA.
XX
AC ADE59630;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein XP_008249, SEQ ID NO 5526.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; XP_008249.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1836 AA;

Query Match 100.0%; Score 28; DB 7; Length 1836;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1271 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1298

RESULT 5
ADE63029
ID ADE63029 standard; protein; 1836 AA.
XX
AC ADE63029;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein XP_008249, SEQ ID NO 8963.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; XP_008249.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1836 AA;

Query Match 100.0%; Score 28; DB 7; Length 1836;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1271 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1298

RESULT 6
ADQ17412
ID ADQ17412 standard; protein; 1836 AA.
XX
AC ADQ17412;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 229.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression

PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 229; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 1836 AA;

Query Match 100.0%; Score 28; DB 8; Length 1836;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1271 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1298

RESULT 7
ADB78597
ID ADB78597 standard; protein; 1855 AA.
XX
AC ADB78597;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:141.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78636.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 141; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 1855 AA;

Query Match 100.0%; Score 28; DB 7; Length 1855;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1459 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1486

RESULT 8
ADB78607
ID ADB78607 standard; protein; 1950 AA.
XX
AC ADB78607;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:151.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;

PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78646.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 151; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 1950 AA;

Query Match 100.0%; Score 28; DB 7; Length 1950;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1394 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1421

RESULT 9
AAB99678
ID AAB99678 standard; protein; 1951 AA.
XX
AC AAB99678;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human adult form of SCN3A protein sequence SEQ ID NO:67.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA001404.
XX
PR 26-NOV-1999; 99US-0167623P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR N-PSDB; AAH55823.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
PS Disclosure; Page 157-165; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
XX
SQ Sequence 1951 AA;

Query Match 100.0%; Score 28; DB 4; Length 1951;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1395 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1422

RESULT 10
AAB99679
ID AAB99679 standard; protein; 1951 AA.
XX
AC AAB99679;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human neonatal form of SCN3A protein sequence SEQ ID NO:68.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA001404.
XX
PR 26-NOV-1999; 99US-0167623P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR N-PSDB; AAH55824.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA

PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
PS Disclosure; Page 165-172; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
XX
SQ Sequence 1951 AA;

Query Match 100.0%; Score 28; DB 4; Length 1951;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1395 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1422

RESULT 11
ADE59628
ID ADE59628 standard; protein; 1951 AA.
XX
AC ADE59628;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein NP_037251, SEQ ID NO 5524.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; NP_037251.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1951 AA;

Query Match 100.0%; Score 28; DB 7; Length 1951;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1395 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1422

RESULT 12
ADL06576
ID ADL06576 standard; protein; 1951 AA.
XX
AC ADL06576;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) polypeptide #75.
XX
KW Human; tumour-associated antigenic target; TAT; cell death; tumour;
KW cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004016225-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US025892.
XX
PR 19-AUG-2002; 2002US-0404809P.
PR 21-AUG-2002; 2002US-0405645P.
PR 23-SEP-2002; 2002US-0413192P.
PR 15-OCT-2002; 2002US-0419008P.
PR 15-NOV-2002; 2002US-0426847P.
PR 02-JUL-2003; 2003US-0484959P.
XX
PA (GETH) GENENTECH INC.
XX
PI Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;
PI Spencer SD, Wu TD, Zhang Z;
XX
DR WPI; 2004-257144/24.
DR N-PSDB; ADL06499.
XX
PT New antibody that binds to a tumor-associated antigenic target (TAT)
PT polypeptide, useful for preparing a composition for diagnosing or

```
PT   treating cancer.
XX
PS   Claim 2; SEQ ID NO 156; 319pp; English.
XX
CC   The present invention relates to the isolation of human tumour-associated
CC   antigenic target (TAT) polynucleotide and polypeptide sequences. Also
CC   disclosed is an antibody that binds to a TAT polypeptide. The antibody is
CC   a monoclonal antibody, an antibody fragment, a chimeric antibody or a
CC   humanised antibody. It is conjugated to a growth inhibitory agent. It is
CC   produced in bacteria or in CHO cells and induces death of a cell to which
CC   it binds. The antibody is useful for preparing a composition for
CC   diagnosing or treating tumours and cancer. The present sequence
CC   represents a human TAT polypeptide of the invention.
XX
SQ   Sequence 1951 AA;

  Query Match             100.0%;  Score 28;  DB 8;  Length 1951;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1395 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1422


RESULT 13
AAE20511
ID   AAE20511 standard; protein; 1962 AA.
XX
AC   AAE20511;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel protein #2.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   medical disorder.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 981
FT                   /note= "Encoded by MTG"
FT   Misc-difference 1056
FT                   /note= "Encoded by RCA"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US025650.
XX
PR   16-AUG-2000; 2000US-0225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   N-PSDB; AAD32840.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders.
XX
PS   Claim 1; Page 37-41; 83pp; English.
XX
CC   The present sequence is novel human protein (NHP), ion channel protein.
CC   NHP share structural similarity with mammalian sodium channel proteins
CC   particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC   are useful as hybridisation probes for screening libraries and assessing
CC   gene expression patterns. Sequences derived from regions adjacent to the
CC   intron/exon boundaries of NHP gene can be used to design primers for use
CC   in amplification assays to detect mutations within the exons, splice
CC   sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC   nucleotide sequences are useful for drug screening effective in the
CC   treatment of symptomatic or phenotypic manifestations of perturbing the
CC   normal function of NHP in the body, and nucleotide constructs encoding
CC   NHP products are useful to genetically engineer host cells to express NHP
CC   products in vivo. These genetically engineered cells function as
CC   bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC   peptide, or a NHP fusion protein to the body. Nucleotide construct
CC   encoding NHP products are also useful in gene therapy for modulating NHP
CC   expression and to produce genetically engineered host cells to express
CC   NHP products in vivo. NHP nucleotide sequences may also be used as part
CC   of ribozyme and/or triple helix sequences that are useful for NHP gene
CC   regulation. The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases
XX
SQ   Sequence 1962 AA;

  Query Match             100.0%;  Score 28;  DB 5;  Length 1962;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1448 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1475


RESULT 14
AAE20516
ID   AAE20516 standard; protein; 1973 AA.
XX
AC   AAE20516;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel protein #7.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   medical disorder.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 992
FT                   /note= "Encoded by MTG"
FT   Misc-difference 1067
FT                   /note= "Encoded by RCA"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US025650.
XX
PR   16-AUG-2000; 2000US-0225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   N-PSDB; AAD32845.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders.
XX
PS   Claim 1; Page 64-68; 83pp; English.
```

```
XX
CC   The present sequence is novel human protein (NHP), ion channel protein.
CC   NHP share structural similarity with mammalian sodium channel proteins
CC   particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC   are useful as hybridisation probes for screening libraries and assessing
CC   gene expression patterns. Sequences derived from regions adjacent to the
CC   intron/exon boundaries of NHP gene can be used to design primers for use
CC   in amplification assays to detect mutations within the exons, splice
CC   sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC   nucleotide sequences are useful for drug screening effective in the
CC   treatment of symptomatic or phenotypic manifestations of perturbing the
CC   normal function of NHP in the body, and nucleotide constructs encoding
CC   NHP products are useful to genetically engineer host cells to express NHP
CC   products in vivo. These genetically engineered cells function as
CC   bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC   peptide, or a NHP fusion protein to the body. Nucleotide construct
CC   encoding NHP products are also useful in gene therapy for modulating NHP
CC   expression and to produce genetically engineered host cells to express
CC   NHP products in vivo. NHP nucleotide sequences may also be used as part
CC   of ribozyme and/or triple helix sequences that are useful for NHP gene
CC   regulation. The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases
XX
SQ   Sequence 1973 AA;

  Query Match             100.0%;  Score 28;  DB 5;  Length 1973;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1459 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1486


RESULT 15
ABR83185
ID   ABR83185 standard; protein; 1981 AA.
XX
AC   ABR83185;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human SCN1A splice variant -84P:SCN1ADELp654-681.
XX
KW   SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
KW   neuroprotective; anesthetic; cytostatic; cerebroprotective; cardiant;
KW   hypotensive; gene therapy; human; splice variant.
XX
OS   Homo sapiens.
XX
PN   WO2003072751-A2.
XX
PD   04-SEP-2003.
XX
PF   25-FEB-2003; 2003WO-US006010.
XX
PR   25-FEB-2002; 2002US-0359382P.
XX
PA   (UYVA-) UNIV VANDERBILT.
XX
PI   George AL,  Lossin C;
XX
DR   WPI; 2003-712725/67.
DR   N-PSDB; ACF57880.
XX
PT   Recombinantly expressed sodium channel type 1 alpha subunit, useful in
PT   screening for modulators, for treating e.g. epilepsy.
XX
PS   Disclosure; Page 162-169; 176pp; English.
XX
CC   The invention relates to a recombinantly expressed and isolated human
CC   SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
CC   incorporated into a cell, is used to screen for specific modulators,
CC   potentially useful as anticonvulsant, antiepileptic, neuroprotective,
CC   analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
CC   epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
CC   motor endplate diseases, hypertension, congestive heart failure and
CC   muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
CC   and metastatic cancer cell lines). These activities can also be provided
CC   by gene therapy vectors that express (I) or the modulators. The
CC   modulators, also antibodies directed against (I), are used to detect
CC   sodium channel polypeptides. The present sequence represents a human
CC   SCN1A splice variant 84P:SCN1ADELp654-681
XX
SQ   Sequence 1981 AA;

  Query Match             100.0%;  Score 28;  DB 7;  Length 1981;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1431 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1458


RESULT 16
AAE20510
ID   AAE20510 standard; protein; 1998 AA.
XX
AC   AAE20510;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel protein #1.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   medical disorder.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 981
FT                   /note= "Encoded by MTG"
FT   Misc-difference 1056
FT                   /note= "Encoded by RCA"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US025650.
XX
PR   16-AUG-2000; 2000US-0225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   N-PSDB; AAD32839.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders.
XX
PS   Claim 1; Page 30-34; 83pp; English.
XX
CC   The present sequence is novel human protein (NHP), ion channel protein.
CC   NHP share structural similarity with mammalian sodium channel proteins
CC   particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC   are useful as hybridisation probes for screening libraries and assessing
CC   gene expression patterns. Sequences derived from regions adjacent to the
```

CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or triple helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
SQ Sequence 1998 AA;

Query Match 100.0%; Score 28; DB 5; Length 1998;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1448 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1475

RESULT 17
ABR83184
ID ABR83184 standard; protein; 1998 AA.
XX
AC ABR83184;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human SCN1A splice variant -33P:SCN1ADELp671-681.
XX
KW SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
KW neuroprotective; anesthetic; cytostatic; cerebroprotective; cardiant;
KW hypotensive; gene therapy; human; splice variant.
XX
OS Homo sapiens.
XX
PN WO2003072751-A2.
XX
PD 04-SEP-2003.
XX
PF 25-FEB-2003; 2003WO-US006010.
XX
PR 25-FEB-2002; 2002US-0359382P.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI George AL, Lossin C;
XX
DR WPI; 2003-712725/67.
DR N-PSDB; ACF57879.
XX
PT Recombinantly expressed sodium channel type 1 alpha subunit, useful in
PT screening for modulators, for treating e.g. epilepsy.
XX
PS Disclosure; Page 148-156; 176pp; English.
XX
CC The invention relates to a recombinantly expressed and isolated human
CC SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
CC incorporated into a cell, is used to screen for specific modulators,
CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,
CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
CC motor endplate diseases, hypertension, congestive heart failure and
CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
CC and metastatic cancer cell lines). These activities can also be provided
CC by gene therapy vectors that express (I) or the modulators. The
CC modulators, also antibodies directed against (I), are used to detect
CC sodium channel polypeptides. The present sequence represents a human
CC SCN1A splice variant 33P:SCN1ADELp671-681 encoding cDNA
XX
SQ Sequence 1998 AA;

Query Match 100.0%; Score 28; DB 7; Length 1998;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1448 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1475

RESULT 18
ABB06026
ID ABB06026 standard; protein; 1999 AA.
XX
AC ABB06026;
XX
DT 10-MAY-2002 (first entry)
XX
DE Human sodium channel SCN1A protein SEQ ID NO:2.
XX
KW Human; sodium channel; SCN1A; chromosome 2q24;
KW familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
OS Homo sapiens.
XX
PN WO200196552-A1.
XX
PD 20-DEC-2001.
XX
PF 12-JUN-2001; 2001WO-JP004956.
XX
PR 13-JUN-2000; 2000JP-00177540.
PR 13-JUN-2000; 2000JP-00177544.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Kanazawa I, Goto J, Jeong S;
XX
DR WPI; 2002-098066/13.
DR N-PSDB; ABL39689.
XX
PT Human sodium channels SCN1A and SCN3A and encoded genes, useful in
PT studying physiological mechanism in which excitant cells participate and
PT causes of diseases and developing drugs for motor endplate disease.
XX
PS Claim 1; Page 40-49; 88pp; Japanese.
XX
CC The present invention describes human sodium channels SCN1A and SCN3A.
CC The present sequence represents the human sodium channel SCN1A. SCN1A and
CC SCN3A have been located to the human chromosome 2 long arm, positions
CC 2q24 and 2q24-31 respectively. The sodium channel proteins are useful in
CC studying the physiological mechanism in which excitant cells participate
CC and cause human diseases, and in developing remedies for e.g. familial
CC hypercalcaemic periodic paralysis of extremities and motor endplate
CC disease
XX
SQ Sequence 1999 AA;

Query Match 100.0%; Score 28; DB 5; Length 1999;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||

```
Db       1449 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1476


RESULT 19
ABB06027
ID   ABB06027 standard; protein; 2000 AA.
XX
AC   ABB06027;
XX
DT   10-MAY-2002  (first entry)
XX
DE   Human sodium channel SCN3A protein SEQ ID NO:4.
XX
KW   Human; sodium channel; SCN3A; chromosome 2q24-31;
KW   familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
OS   Homo sapiens.
XX
PN   WO200196552-A1.
XX
PD   20-DEC-2001.
XX
PF   12-JUN-2001; 2001WO-JP004956.
XX
PR   13-JUN-2000; 2000JP-00177540.
PR   13-JUN-2000; 2000JP-00177544.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Kanazawa I,  Goto J,  Jeong S;
XX
DR   WPI; 2002-098066/13.
DR   N-PSDB; ABL39690.
XX
PT   Human sodium channels SCN1A and SCN3A and encoded genes, useful in
PT   studying physiological mechanism in which excitant cells participate and
PT   causes of diseases and developing drugs for motor endplate disease.
XX
PS   Claim 2; Page 72-81; 88pp; Japanese.
XX
CC   The present invention describes human sodium channels SCN1A and SCN3A.
CC   The present sequence represents the human sodium channel SCN3A. SCN1A and
CC   SCN3A have been located to the human chromosome 2 long arm, positions
CC   2q24 and 2q24-31 respectively. The sodium channel proteins are useful in
CC   studying the physiological mechanism in which excitant cells participate
CC   and cause human diseases, and in developing remedies for e.g. familial
CC   hypercalcaemic periodic paralysis of extremities and motor endplate
CC   disease
XX
SQ   Sequence 2000 AA;

  Query Match             100.0%;  Score 28;  DB 5;  Length 2000;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1444 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1471


RESULT 20
ADK81762
ID   ADK81762 standard; protein; 2000 AA.
XX
AC   ADK81762;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human Nav1.3 protein.
XX
KW   Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW   diabetic neuropathy; arthritic pain; migraine headache;
KW   infantile epilepsy; ataxia.
XX
OS   Homo sapiens.
XX
PN   WO2004016754-A2.
XX
PD   26-FEB-2004.
XX
PF   14-AUG-2003; 2003WO-US025465.
XX
PR   14-AUG-2002; 2002US-0403416P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Roberds SL;
XX
DR   WPI; 2004-203785/19.
DR   N-PSDB; ADK81761.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   Nav1.3, useful for useful for treating a disease or condition associated
PT   with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT   disorder, or ataxia.
XX
PS   Disclosure; SEQ ID NO 9096; 417pp; English.
XX
CC   The present invention relates to an antisense compound targeted to a
CC   nucleic acid molecule encoding Nav1.3, where the antisense compound
CC   specifically hybridizes with and inhibits the expression of Nav1.3. The
CC   compound and composition are useful for treating a disease or condition
CC   associated with Nav1.3, e.g. pain including but not limited to
CC   neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC   diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC   pain from burns, migraine headache, cluster headache, mild-to-moderate
CC   headache; seizure disorder such as childhood seizure disorder, including
CC   but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC   sequence represents human Nav1.3 protein.
XX
SQ   Sequence 2000 AA;

  Query Match             100.0%;  Score 28;  DB 8;  Length 2000;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1444 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1471


RESULT 21
AAB99676
ID   AAB99676 standard; protein; 2005 AA.
XX
AC   AAB99676;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human adult form of SCN2A protein sequence SEQ ID NO:35.
XX
KW   Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW   diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW   anticonvulsant; neuroprotective.
XX
OS   Homo sapiens.
XX
PN   WO200138564-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-CA001404.
XX
PR   26-NOV-1999;   99US-0167623P.
XX
PA   (UYMC-) UNIV MCGILL.
```

XX
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR N-PSDB; AAH55793.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
PS Disclosure; Page 123-130; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 4; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1449 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1476

RESULT 22
AAB99677
ID AAB99677 standard; protein; 2005 AA.
XX
AC AAB99677;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human neonatal form of SCN2A protein sequence SEQ ID NO:36.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA001404.
XX
PR 26-NOV-1999; 99US-0167623P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR N-PSDB; AAH55794.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
PS Disclosure; Page 131-138; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 4; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1449 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1476

RESULT 23
ABB83627
ID ABB83627 standard; protein; 2005 AA.
XX
AC ABB83627;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human GEFS+ protein with SCN2A mutation.
XX
KW Human; GEFS+; SCN2A; mutant; mutein;
KW generalized epilepsy with febrile seizure plus.
XX
OS Homo sapiens.
XX
PN JP2002136289-A.
XX
PD 14-MAY-2002.
XX
PF 01-NOV-2000; 2000JP-00334969.
XX
PR 01-NOV-2000; 2000JP-00334969.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (RIKA) RIKAGAKU KENKYUSHO.
XX
DR WPI; 2002-552308/59.
DR N-PSDB; ABQ79201.
XX
PT A human polynucleotide which is complementary to an mRNA transcribed from
PT a generalized epilepsy with febrile seizure plus (GEFS+)-related gene
PT useful for diagnosing GEFS+.
XX
PS Claim 10; Page 29-34; 37pp; Japanese.
XX
CC This invention relates to a human polynucleotide which is complementary
CC to an mRNA transcribed from a "generalized epilepsy with febrile seizure
CC plus" (GEFS+)-related gene. The gene is useful for diagnosing GEFS+. The
CC present sequence represents the human GEFS+ protein sequence with SCN2A
CC mutation
XX
SQ Sequence 2005 AA;

```
  Query Match             100.0%;  Score 28;  DB 5;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1449 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1476


RESULT 24
ADB78604
ID   ADB78604 standard; protein; 2005 AA.
XX
AC   ADB78604;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human sodium channel subunit mutant SEQ ID NO:148.
XX
KW   mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW   neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW   antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW   nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW   ion channel dysfunction; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003008574-A1.
XX
PD   30-JAN-2003.
XX
PF   08-JUL-2002; 2002WO-AU000910.
XX
PR   18-JUL-2001; 2001AU-00006452.
PR   05-MAR-2002; 2002AU-00000910.
PR   13-MAY-2002; 2002AU-00002292.
XX
PA   (BION-) BIONOMICS LTD.
PA   (WALL/) WALLACE R W.
XX
PI   Mulley JC,  Harkin LA,  Dibbens LM,  Phillips HA,  Heron SE;
PI   Berkovic SF,  Scheffer IE;
XX
DR   WPI; 2003-239332/23.
DR   N-PSDB; ADB78643.
XX
PT   Identifying predisposition to an ion channel dysfunction, such as
PT   periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT   schizophrenia, anxiety and depression, by detecting encoding-gene
PT   mutation events.
XX
PS   Claim 13; SEQ ID NO 148; 106pp; English.
XX
CC   The invention relates to a novel method for identifying a subject
CC   predisposed to a disorder associated with ion channel dysfunction. The
CC   method comprises ascertaining if at least one of the genes encoding ion
CC   channel subunits (ICS) has undergone a mutation event so that a cDNA
CC   derived from the subject has any of 134 nucleotide sequences. The method
CC   of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC   antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC   neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC   ophthalmological activity. A polynucleotide of the invention acts as an
CC   ion channel agonist, or ion channel antagonist. The methods, isolated
CC   nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC   modulator of an ion channel, cells and genetically modified non-human
CC   animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC   disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC   kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC   myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC   disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC   depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC   pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC   Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC   fibrosis, congenital stationary night blindness and total colour
CC   blindness. The present sequence represents a mutant protein of the
CC   invention. The sequence data for this patent is not represented in the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ   Sequence 2005 AA;

  Query Match             100.0%;  Score 28;  DB 7;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1449 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1476


RESULT 25
ADB78603
ID   ADB78603 standard; protein; 2005 AA.
XX
AC   ADB78603;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human sodium channel subunit mutant SEQ ID NO:147.
XX
KW   mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW   neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW   antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW   nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW   ion channel dysfunction; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003008574-A1.
XX
PD   30-JAN-2003.
XX
PF   08-JUL-2002; 2002WO-AU000910.
XX
PR   18-JUL-2001; 2001AU-00006452.
PR   05-MAR-2002; 2002AU-00000910.
PR   13-MAY-2002; 2002AU-00002292.
XX
PA   (BION-) BIONOMICS LTD.
PA   (WALL/) WALLACE R W.
XX
PI   Mulley JC,  Harkin LA,  Dibbens LM,  Phillips HA,  Heron SE;
PI   Berkovic SF,  Scheffer IE;
XX
DR   WPI; 2003-239332/23.
DR   N-PSDB; ADB78642.
XX
PT   Identifying predisposition to an ion channel dysfunction, such as
PT   periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT   schizophrenia, anxiety and depression, by detecting encoding-gene
PT   mutation events.
XX
PS   Claim 13; SEQ ID NO 147; 106pp; English.
XX
CC   The invention relates to a novel method for identifying a subject
CC   predisposed to a disorder associated with ion channel dysfunction. The
CC   method comprises ascertaining if at least one of the genes encoding ion
CC   channel subunits (ICS) has undergone a mutation event so that a cDNA
CC   derived from the subject has any of 134 nucleotide sequences. The method
CC   of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC   antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC   neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC   ophthalmological activity. A polynucleotide of the invention acts as an
CC   ion channel agonist, or ion channel antagonist. The methods, isolated
```

CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 7; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
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Db       1449 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1476
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Search completed: January 27, 2005, 17:45:16
Job time : 87.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:36:05 ; Search time 17 Seconds
(without alignments)
158.475 Million cell updates/sec

Title: US-10-608-584-19
Perfect score: 28
Sequence: 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	100.0	1835	2	I54323	sodium channel alp
2	28	100.0	1836	2	I64893	sodium channel alp
3	28	100.0	1836	2	JS0648	sodium channel alp
4	28	100.0	1836	2	I51964	sodium channel alp
5	28	100.0	1840	1	CHRTM1	sodium channel pro
6	28	100.0	1951	2	S00320	sodium channel pro
7	28	100.0	1983	2	A60054	sodium channel pro
8	28	100.0	2005	2	A46269	sodium channel alp
9	28	100.0	2005	2	B25019	sodium channel pro
10	28	100.0	2009	2	A25019	sodium channel pro
11	25	89.3	1976	2	I56555	sodium channel pro
12	25	89.3	2016	2	A38195	sodium channel pro
13	21	75.0	295	2	A56595	sodium channel alp
14	21	75.0	1689	2	S72467	sodium channel pro
15	21	75.0	1699	2	T31340	voltage-gated sodi
16	21	75.0	1765	2	T42388	sodium channel alp
17	21	75.0	1784	2	T43167	sodium channel pro
18	21	75.0	1820	2	A33299	sodium channel pro
19	21	75.0	1977	2	S54771	sodium channel alp
20	21	75.0	2019	2	A33996	sodium channel pro
21	21	75.0	2108	2	S72458	sodium channel pro
22	18	64.3	2049	2	T43161	sodium channel pro
23	17	60.7	1321	2	A60165	sodium channel pro
24	17	60.7	1810	2	T31092	probable voltage-g
25	15	53.6	1820	1	CHEE	sodium channel pro
26	13	46.4	1993	2	T30902	sodium channel SCA
27	12	42.9	1695	2	JE0084	voltage-gated sodi
28	12	42.9	1739	2	A48298	sodium channel hom
29	8	28.6	1522	2	JC1101	sodium channel pro
30	7	25.0	260	2	G81290	probable capsule p
31	7	25.0	274	2	E83837	hypothetical prote
32	7	25.0	351	2	A69808	H+/Ca2+ exchanger
33	7	25.0	399	2	E84964	hypothetical prote
34	7	25.0	491	2	T23524	hypothetical prote
35	7	25.0	494	1	O4HUA6	coumarin 7-hydroxy
36	7	25.0	542	2	F90457	hypothetical prote
37	7	25.0	1957	2	S68453	sodium channel pro
38	6	21.4	22	2	S17303	tegumental glycopr
39	6	21.4	118	2	C90105	60S ribosomal prot
40	6	21.4	129	2	T25141	hypothetical prote
41	6	21.4	130	2	C90503	conserved hypothet
42	6	21.4	153	2	S52605	probable membrane
43	6	21.4	155	2	A91055	hypothetical prote
44	6	21.4	155	2	D85899	hypothetical prote
45	6	21.4	162	2	T13574	NADH2 dehydrogenas
46	6	21.4	164	2	F65031	hypothetical prote
47	6	21.4	164	2	H71175	hypothetical prote
48	6	21.4	182	1	R5MX6	ribosomal protein
49	6	21.4	182	2	A45553	22K surface membra
50	6	21.4	184	2	B90592	hypothetical prote
51	6	21.4	192	2	S09506	hypothetical prote
52	6	21.4	218	2	S43591	M04D8.4 protein -
53	6	21.4	220	2	B64681	nicotinamide monon
54	6	21.4	220	2	B71832	nicotinamide monon
55	6	21.4	221	2	D86878	hypothetical prote
56	6	21.4	237	2	S64315	hypothetical prote
57	6	21.4	240	2	H84497	probable replicati
58	6	21.4	248	2	S57461	H+-transporting tw
59	6	21.4	251	2	S38811	hypothetical prote
60	6	21.4	254	2	E97242	signal peptidase t
61	6	21.4	256	2	AG0413	probable ABC trans
62	6	21.4	258	2	E72319	flagellar biosynth
63	6	21.4	259	2	A83294	probable permease
64	6	21.4	261	2	AD1721	hypothetical prote
65	6	21.4	261	2	F90506	hypothetical prote
66	6	21.4	279	2	E70322	hypothetical prote
67	6	21.4	282	2	C84114	UDP-glucose 4-epim
68	6	21.4	286	2	I46855	voltage-gated pota
69	6	21.4	314	2	T32672	hypothetical prote
70	6	21.4	316	2	S46055	probable membrane
71	6	21.4	317	2	A71698	hypothetical prote
72	6	21.4	322	2	E81279	enterochelin uptak
73	6	21.4	322	2	D96921	oligopeptide trans
74	6	21.4	331	1	O4HUPB	cytochrome P450 2A
75	6	21.4	333	2	B84195	hypothetical prote
76	6	21.4	335	2	G83598	cell division prot
77	6	21.4	336	2	F75320	WD-repeat family p
78	6	21.4	339	2	S61020	probable membrane
79	6	21.4	340	2	S41752	UDP-3-O-[3-hydroxy
80	6	21.4	340	2	AE0129	UDP-3-O-[3-hydroxy
81	6	21.4	341	2	AD0530	UDP-3-O-[3-hydroxy
82	6	21.4	341	2	S13729	UDP-3-O-[3-hydroxy
83	6	21.4	341	2	E85502	hypothetical prote
84	6	21.4	341	2	E90651	hypothetical prote
85	6	21.4	341	2	B37083	Ssc protein - Salm
86	6	21.4	345	2	T12354	NADH2 dehydrogenas
87	6	21.4	351	2	E97768	microcin C7 self-i
88	6	21.4	365	2	AF3119	hypothetical prote
89	6	21.4	374	2	A98168	hypothetical prote
90	6	21.4	375	2	D82894	heat shock protein
91	6	21.4	381	2	S59093	ubiquinol-cytochro
92	6	21.4	398	2	D75093	macrolide-efflux d
93	6	21.4	406	2	T23934	hypothetical prote
94	6	21.4	409	2	AG0235	probable sugar tra
95	6	21.4	409	2	T47026	hypothetical prote
96	6	21.4	411	2	E84949	tetrahydrofolylpol
97	6	21.4	434	2	AH1990	hypothetical prote
98	6	21.4	437	2	G82777	glutamate symport
99	6	21.4	444	2	F71916	probable lipopolys
100	6	21.4	468	2	S75389	probable phenylala

ALIGNMENTS

RESULT 1
I54323
sodium channel alpha subunit - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C;Accession: I54323
R;McClatchey, A.I.; Lin, C.S.; Wang, J.; Hoffman, E.P.; Rojas, C.; Gusella, J.F.
Hum. Mol. Genet. 1, 521-527, 1992
A;Title: The genomic structure of the human skeletal muscle sodium channel gene.
A;Reference number: I54323; MUID:93338444; PMID:1339144
A;Accession: I54323
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1835 <RES>
A;Cross-references: GB:L01983; NID:g337992; PIDN:AAA75557.1; PID:g908809
C;Genetics:
A;Gene: GDB:SCN4A
A;Cross-references: GDB:125181; OMIM:170500
A;Map position: 17q23.1-17q25.3
A;Introns: 91/3; 131/2; 161/2; 204/2; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/3; 6
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 100.0%; Score 28; DB 2; Length 1835;
Best Local Similarity 100.0%; Pred. No. 3.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1271 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1298

RESULT 2
I64893
sodium channel alpha subunit - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: I64893
R;George, A.L.
Ann. Neurol. 31, 131-137, 1992
A;Title: Primary structure of the adult human skeletal muscle voltage-dependent sodium c
A;Reference number: I51964; MUID:92246457; PMID:1315496
A;Accession: I64893
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1836 <RES>
A;Cross-references: UNIPROT:P35499; GB:M81758; NID:g338212; PIDN:AAA60554.1; PID:g338213
C;Genetics:
A;Gene: SkM1
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 100.0%; Score 28; DB 2; Length 1836;
Best Local Similarity 100.0%; Pred. No. 3.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1271 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1298

RESULT 3
JS0648
sodium channel alpha chain - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JS0648; A42099
R;Wang, J.; Rojas, C.V.; Zhou, J.; Schwartz, L.S.; Nicholas, H.; Hoffmann, E.P.
Biochem. Biophys. Res. Commun. 182, 794-801, 1992
A;Title: Sequence and genomic structure of the human adult skeletal muscle sodium channe
A;Reference number: JS0648; MUID:92134303; PMID:1310396
A;Accession: JS0648
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1836 <WAN>
A;Cross-references: UNIPROT:P35499
A;Note: 861-Asp was also found as the result of polymorphism
R;McClatchey, A.I.; Van den Bergh, P.; Pericak-Vance, M.A.; Raskind, W.; Verellen, C.; Mc
Cell 68, 769-774, 1992
A;Title: Temperature-sensitive mutations in the III-IV cytoplasmic loop region of the s
A;Reference number: A42099; MUID:92154689; PMID:1310898
A;Accession: A42099
A;Molecule type: DNA
A;Residues: 1299-1351 <MCC>
A;Cross-references: GB:S82622; NID:g245611; PIDN:AAB21450.1; PID:g245612
A;Experimental source: skeletal muscle
A;Note: sequence extracted from NCBI backbone (NCBIN:82622, NCBIP:82623)
C;Genetics:
A;Gene: GDB:SCN4A
A;Cross-references: GDB:125181; OMIM:170500
A;Map position: 17q23.1-17q25.3
C;Superfamily: sodium channel protein
C;Keywords: duplication; glycoprotein; phosphoprotein; transmembrane protein
F;129-150/Domain: transmembrane #status predicted <TR1>
F;159-178/Domain: transmembrane #status predicted <TR2>
F;191-210/Domain: transmembrane #status predicted <TR3>
F;217-236/Domain: transmembrane #status predicted <TR4>
F;253-266/Domain: transmembrane #status predicted <TR5>
F;424-449/Domain: transmembrane #status predicted <TR6>
F;574-597/Domain: transmembrane #status predicted <RI1>
F;609-632/Domain: transmembrane #status predicted <RI2>
F;641-660/Domain: transmembrane #status predicted <RI3>
F;667-686/Domain: transmembrane #status predicted <RI4>
F;702-724/Domain: transmembrane #status predicted <RI5>
F;777-802/Domain: transmembrane #status predicted <RI6>
F;1027-1049/Domain: transmembrane #status predicted <II1>
F;1064-1089/Domain: transmembrane #status predicted <II2>
F;1096-1116/Domain: transmembrane #status predicted <II3>
F;1122-1143/Domain: transmembrane #status predicted <II4>
F;1163-1184/Domain: transmembrane #status predicted <II5>
F;1269-1295/Domain: transmembrane #status predicted <II6>
F;1349-1372/Domain: transmembrane #status predicted <VS1>
F;1384-1407/Domain: transmembrane #status predicted <VS2>
F;1414-1437/Domain: transmembrane #status predicted <VS3>
F;1447-1469/Domain: transmembrane #status predicted <VS4>
F;1485-1507/Domain: transmembrane #status predicted <VS5>
F;1574-1598/Domain: transmembrane #status predicted <VS6>
F;21,149,220,378,415,1019,1130,1242,1313,1721,1826/Binding site: phosphate (Thr) (covaler
F;56,251,513,653,1511,1746/Binding site: phosphate (Ser) (covalent) (by protein kinase A)
F;214,288,291,297,303,315,321,333,362,507,702,961,1191,1205/Binding site: carbohydrate (
F;246,670,725,850,950,1127,1195,1328/Binding site: phosphate (Ser) (covalent) (by proteir
F;387,457/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicte

Query Match 100.0%; Score 28; DB 2; Length 1836;
Best Local Similarity 100.0%; Pred. No. 3.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||||||||
Db 1271 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1298

RESULT 4
I51964
sodium channel alpha chain SCN4A, skeletal muscle - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I51964
R;George, A.L.
Ann. Neurol. 31, 131-137, 1992
A;Title: Primary structure of the adult human skeletal muscle voltage-dependent sodium ch
A;Reference number: I51964; MUID:92246457; PMID:1315496
A;Accession: I51964

```
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1836 <RES>
A;Cross-references: UNIPROT:P35499; GB:L04236; NID:g292485; PIDN:AAB59624.1; PID:g292487
C;Genetics:
A;Gene: GDB:SCN4A
A;Cross-references: GDB:125181; OMIM:170500
A;Map position: 17q23.1-17q25.3
A;Introns: 91/3; 131/2; 161/2; 204/2; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/3; 6
C;Superfamily: sodium channel protein
C;Keywords: duplication; skeletal muscle

  Query Match             100.0%;  Score 28;  DB 2;  Length 1836;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1271 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1298


RESULT 5
CHRTM1
sodium channel protein mu1 alpha chain, skeletal muscle - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: JN0007
R;Trimmer, J.S.; Cooperman, S.S.; Tomiko, S.A.; Zhou, J.; Crean, S.M.; Boyle, M.B.; Kall
Neuron 3, 33-49, 1989
A;Title: Primary structure and functional expression of a mammalian skeletal muscle sodi
A;Reference number: JN0007; MUID:90148778; PMID:2559760
A;Accession: JN0007
A;Molecule type: mRNA
A;Residues: 1-1840 <TRI>
A;Cross-references: UNIPROT:P15390; GB:M26643; NID:g205651; PIDN:AAA41682.1; PID:g205652
C;Comment: Action potentials propagated by skeletal muscle sodium channels are responsib
C;Comment: This heavily glycosylated protein contains four homologous domains, each of w
C;Comment: This protein is distinct from but related to sodium channel proteins isolated
C;Superfamily: sodium channel protein
C;Keywords: duplication; glycoprotein; ion transport; neuromuscular junction; phosphopro
F;120-458,561-813,1013-1305,1335-1611/Region: duplication
F;56,251,1321,1504/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #
F;214,288,291,297,303,309,315,327,356,502,696,954,1184,1198,1563,1702/Binding site: carb

  Query Match             100.0%;  Score 28;  DB 1;  Length 1840;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1264 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1291


RESULT 6
S00320
sodium channel protein III - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S00320
R;Kayano, T.; Noda, M.; Flockerzi, V.; Takahashi, H.; Numa, S.
FEBS Lett. 228, 187-194, 1988
A;Title: Primary structure of rat brain sodium channel III deduced from the cDNA sequenc
A;Reference number: S00320; MUID:88137594; PMID:2449363
A;Accession: S00320
A;Molecule type: mRNA
A;Residues: 1-1951 <KAY>
A;Cross-references: UNIPROT:P08104; EMBL:Y00766; NID:g57210; PIDN:CAA68735.1; PID:g57211
A;Note: 270-Ile, 278-Leu, 355-Thr, 513-Lys, and 1059-Arg were also found
C;Superfamily: sodium channel protein
C;Keywords: duplication; transmembrane protein

  Query Match             100.0%;  Score 28;  DB 2;  Length 1951;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1395 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1422


RESULT 7
A60054
sodium channel protein IIIb, long form - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60054; B44824
R;Joho, R.H.; Moorman, J.R.; VanDongen, A.M.J.; Kirsch, G.E.; Silberberg, H.; Schuster,
Brain Res. Mol. Brain Res. 7, 105-113, 1990
A;Title: Toxin and kinetic profile of rat brain type III sodium channels expressed in Xe
A;Reference number: A60054; MUID:90251117; PMID:2160038
A;Accession: A60054
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1983 <JOH>
A;Cross-references: UNIPROT:Q64243
R;Schaller, K.L.; Krzemien, D.M.; McKenna, N.M.; Caldwell, J.H.
J. Neurosci. 12, 1370-1381, 1992
A;Title: Alternatively spliced sodium channel transcripts in brain and muscle.
A;Reference number: A44824; MUID:92211397; PMID:1313493
A;Accession: B44824
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 611-662 <SCH>
A;Cross-references: GB:S97388; NID:g248225; PIDN:AAB21984.1; PID:g248226
A;Experimental source: skeletal muscle
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:97388, NCBIP:97391)
C;Superfamily: sodium channel protein
C;Keywords: duplication; glycoprotein; ion transport; sodium channel; transmembrane prot

  Query Match             100.0%;  Score 28;  DB 2;  Length 1983;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1427 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1454


RESULT 8
A46269
sodium channel alpha chain HBA - human
C;Species: Homo sapiens (man)
C;Date: 20-Oct-1993 #sequence_revision 18-Nov-1994 #text_change 21-Nov-1997
C;Accession: A46269
R;Ahmed, C.M.; Ware, D.H.; Lee, S.C.; Patten, C.D.; Ferrer-Montiel, A.V.; Schinder, A.F.
Proc. Natl. Acad. Sci. U.S.A. 89, 8220-8224, 1992
A;Title: Primary structure, chromosomal localization, and functional expression of a vol
A;Reference number: A46269; MUID:92390418; PMID:1325650
A;Accession: A46269
A;Molecule type: mRNA
A;Residues: 1-2005 <AHM>
A;Cross-references: GB:M94055
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:113082)
C;Genetics:
A;Map position: 2q23-q24.3
C;Superfamily: sodium channel protein
C;Keywords: duplication

  Query Match             100.0%;  Score 28;  DB 2;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
```

```
Db       1449 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1476

RESULT 9
B25019
sodium channel protein II - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: B25019; S24804
R;Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H
Nature 320, 188-192, 1986
A;Title: Existence of distinct sodium channel messenger RNAs in rat brain.
A;Reference number: A93377; MUID:86146901; PMID:3754035
A;Accession: B25019
A;Molecule type: mRNA
A;Residues: 1-2005 <NOD>
A;Cross-references: UNIPROT:Q63509
A;Experimental source: brain
R;Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
submitted to the EMBL Data Library, August 1991
A;Description: Developmentally regulated RNA splicing of rat brain sodium channel mRNAs.
A;Reference number: S24803
A;Accession: S24804
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 183-188,'D',190-305 <SAR>
A;Cross-references: EMBL:X61149; NID:g57074; PIDN:CAA43458.1; PID:g57076
C;Superfamily: sodium channel protein
C;Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-g

  Query Match              100.0%;  Score 28;  DB 2;  Length 2005;
  Best Local Similarity    100.0%;  Pred. No. 3.7e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1449 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1476

RESULT 10
A25019
sodium channel protein I - rat
N;Alternate names: sodium channel protein A
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A25019; S40783; I84764
R;Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H
Nature 320, 188-192, 1986
A;Title: Existence of distinct sodium channel messenger RNAs in rat brain.
A;Reference number: A93377; MUID:86146901; PMID:3754035
A;Accession: A25019
A;Molecule type: mRNA
A;Residues: 1-2009 <NOD>
A;Cross-references: UNIPROT:P04774; GB:X03638; NID:g57216; PIDN:CAA27286.1; PID:g57217
A;Experimental source: brain
R;Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
Nucleic Acids Res. 19, 5673-5679, 1991
A;Title: Developmentally regulated alternative RNA splicing of rat brain sodium channel
A;Reference number: S40782; MUID:92051314; PMID:1658739
A;Accession: S40783
A;Molecule type: DNA
A;Residues: 177-253 <SAR>
R;Noda, M.; Numa, S.
J. Recept. Res. 7, 467-497, 1987
A;Title: Structure and function of sodium channel.
A;Reference number: I50536; MUID:87311395; PMID:2442385
A;Accession: I84764
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2009 <RES>
A;Cross-references: GB:M22253; NID:g1041088; PIDN:AAA79965.1; PID:g1041089
C;Superfamily: sodium channel protein
C;Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-g

  Query Match              100.0%;  Score 28;  DB 2;  Length 2009;
  Best Local Similarity    100.0%;  Pred. No. 3.7e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1459 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1486

RESULT 11
I56555
sodium channel protein 6 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56555
R;Schaller, K.L.; Krzemien, D.M.; Yarowsky, P.J.; Krueger, B.K.; Caldwell, J.H.
J. Neurosci. 15, 3231-3242, 1995
A;Title: A novel, abundant sodium channel expressed in neurons and glia.
A;Reference number: I56555; MUID:95271284; PMID:7751906
A;Accession: I56555
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1976 <RES>
A;Cross-references: UNIPROT:Q63541; GB:L39018; NID:g829033; PIDN:AAC42059.1; PID:g829034
C;Genetics:
A;Gene: SCP6
C;Superfamily: sodium channel protein
C;Keywords: duplication

  Query Match              89.3%;  Score 25;  DB 2;  Length 1976;
  Best Local Similarity    100.0%;  Pred. No. 3.7e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1439 YFVIFIIFGSFFTLNLFIGVIIDNF 1463

RESULT 12
A38195
sodium channel protein hHI, cardiac - human
N;Alternate names: tetrodotoxin-insensitive, voltage-dependent sodium channel, TTX-I Na
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A38195
R;Gellens, M.E.; George Jr., A.L.; Chen, L.Q.; Chahine, M.; Horn, R.; Barchi, R.L.; Kall
Proc. Natl. Acad. Sci. U.S.A. 89, 554-558, 1992
A;Title: Primary structure and functional expression of the human cardiac tetrodotoxin-i
A;Reference number: A38195; MUID:92115699; PMID:1309946
A;Accession: A38195
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-2016 <GEL>
A;Cross-references: UNIPROT:Q14524; GB:M77235; NID:g184038; PIDN:AAA58644.1; PID:g184039
A;Experimental source: heart
C;Superfamily: sodium channel protein
C;Keywords: cardiac muscle; duplication; glycoprotein; heart; ion transport; sodium chanr

  Query Match              89.3%;  Score 25;  DB 2;  Length 2016;
  Best Local Similarity    100.0%;  Pred. No. 3.7e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1449 YFVIFIIFGSFFTLNLFIGVIIDNF 1473

RESULT 13
A56595
sodium channel alpha chain hscp - tobacco budworm (fragment)
C;Species: Heliothis virescens (tobacco budworm)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
```

C;Accession: A56595
R;Taylor, M.F.; Heckel, D.G.; Brown, T.M.; Kreitman, M.E.; Black, B.
Insect Biochem. Mol. Biol. 23, 763-775, 1993
A;Title: Linkage of pyrethroid insecticide resistance to a sodium channel locus in the t
A;Reference number: A56595; MUID:93386183; PMID:8397035
A;Accession: A56595
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-295 <TAY>
A;Cross-references: UNIPROT:Q25178; GB:U24236
A;Experimental source: pyrethroid resistant strain PEG-87
A;Note: authors translated the codons GGC for residue 122 as Ala, GTA for residue 238 as
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 75.0%; Score 21; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 7.2e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||
Db 94 FIIFGSFFTLNLFIGVIIDNF 114

RESULT 14
S72467
sodium channel protein para-type alpha chain - German cockroach (strain CSMA) (fragment)
C;Species: Blattella germanica (German cockroach)
A;Variety: strain CSMA
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: S72467; S72487
R;Miyazaki, M.; Ohyama, K.; Dunlap, D.Y.; Matsumura, F.
submitted to the EMBL Data Library, September 1996
A;Description: Cloning and sequencing of the para-type sodium channel gene from suscepti
A;Reference number: S72467
A;Accession: S72467
A;Molecule type: mRNA
A;Residues: 1-1689 <MIY>
A;Cross-references: UNIPROT:Q93135; EMBL:U71083; NID:g1633647; PIDN:AAB82037.1; PID:g163
R;Miyazaki, M.; Ohyama, K.; Dunlap, D.Y.; Matsumura, F.
Mol. Gen. Genet. 252, 61-68, 1996
A;Title: Cloning and sequencing of the para-type sodium channel gene from susceptible an
A;Reference number: S72487; MUID:96397510; PMID:8804404
A;Accession: S72487
A;Molecule type: mRNA
A;Residues: 711-819 <MIW>
A;Cross-references: EMBL:U71083
C;Superfamily: sodium channel protein
C;Keywords: duplication; sodium channel; transmembrane protein

Query Match 75.0%; Score 21; DB 2; Length 1689;
Best Local Similarity 100.0%; Pred. No. 3.3e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||
Db 1304 FIIFGSFFTLNLFIGVIIDNF 1324

RESULT 15
T31340
voltage-gated sodium channel homolog - Bdelloura candida
C;Species: Bdelloura candida
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T31340
R;Jeziorski, M.C.; Greenberg, R.M.; Anderson, P.A.
submitted to the EMBL Data Library, March 1997
A;Description: A putative voltage-gated sodium channel from the turbellarian flatworm Bd
A;Reference number: Z21006
A;Accession: T31340
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1699 <JEZ>
A;Cross-references: UNIPROT:O02037; EMBL:U93074; NID:g1947093; PID:g1947094; PIDN:AAC630
C;Genetics:
A;Gene: Na1
C;Superfamily: sodium channel protein

Query Match 75.0%; Score 21; DB 2; Length 1699;
Best Local Similarity 100.0%; Pred. No. 3.3e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||
Db 1231 FIIFGSFFTLNLFIGVIIDNF 1251

RESULT 16
T42388
sodium channel alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42388
R;Dib-Hajj, S.D.; Tyrrell, L.; Black, J.A.; Waxman, S.G.
Proc. Natl. Acad. Sci. U.S.A. 95, 8963-8968, 1998
A;Title: NaN, a novel voltage-gated Na channel, is expressed preferentially in periphera
A;Reference number: Z22149; MUID:98338024; PMID:9671787
A;Accession: T42388
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1765 <DIB>
A;Cross-references: UNIPROT:O88457; EMBL:AF059030; NID:g3372614; PID:g3372615; PIDN:AAC4
A;Experimental source: strain Sprague-Dawley; dorsal root ganglia
A;Note: preferentially expressed in sensory neurons within dorsal root ganglia and trigem
C;Superfamily: sodium channel protein

Query Match 75.0%; Score 21; DB 2; Length 1765;
Best Local Similarity 100.0%; Pred. No. 3.4e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||
Db 1271 FIIFGSFFTLNLFIGVIIDNF 1291

RESULT 17
T43167
sodium channel protein - California market squid
C;Species: Loligo opalescens (California market squid)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43167
R;Rosenthal, J.J.; Gilly, W.F.
Proc. Natl. Acad. Sci. U.S.A. 90, 10026-10030, 1993
A;Title: Amino acid sequence of a putative sodium channel expressed in the giant axon of
A;Reference number: Z22324; MUID:94052096; PMID:8234251
A;Accession: T43167
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1784 <ROS>
A;Cross-references: UNIPROT:Q25377; EMBL:L19979; NID:g349118; PID:g349119; PIDN:AAA16202
A;Experimental source: stellate ganglia
C;Superfamily: sodium channel protein
C;Keywords: ion transport; membrane protein; sodium channel; voltage-gated ion channel

Query Match 75.0%; Score 21; DB 2; Length 1784;
Best Local Similarity 100.0%; Pred. No. 3.4e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FIIFGSFFTLNLFIGVIIDNF 28
||||||||||||||||||||||
Db 1268 FIIFGSFFTLNLFIGVIIDNF 1288

RESULT 18
A33299
sodium channel protein - fruit fly (Drosophila melanogaster) (fragment)

```
C;Species: Drosophila melanogaster
C;Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 21-Nov-1997
C;Accession: A33299
R;Loughney, K.; Kreber, R.; Ganetzky, B.
Cell 58, 1143-1154, 1989
A;Title: Molecular analysis of the para locus, a sodium channel gene in Drosophila.
A;Reference number: A33299; MUID:89376565; PMID:2550145
A;Accession: A33299
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1820 <LOU>
A;Cross-references: GB:M32078; GB:M24285
C;Genetics:
A;Gene: FlyBase:para
A;Cross-references: FlyBase:FBgn0003036
C;Superfamily: sodium channel protein
C;Keywords: duplication; phosphoprotein; transmembrane protein

  Query Match             75.0%;  Score 21;  DB 2;  Length 1820;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 FIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||
Db       1499 FIIFGSFFTLNLFIGVIIDNF 1519


RESULT 19
S54771
sodium channel alpha subunit - human
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54771
R;Klugbauer, N.; Lacinova, L.; Flockerzi, V.; Hofmann, F.
EMBO J. 14, 1084-1090, 1995
A;Title: Structure and functional expression of a new member of the tetrodotoxin-sensiti
A;Reference number: S54771; MUID:95237189; PMID:7720699
A;Accession: S54771
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1977 <KLU>
A;Cross-references: UNIPROT:Q15858; EMBL:X82835; NID:g758109; PIDN:CAA58042.1; PID:g7581
C;Superfamily: sodium channel protein
C;Keywords: duplication

  Query Match             75.0%;  Score 21;  DB 2;  Length 1977;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 FIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||
Db       1429 FIIFGSFFTLNLFIGVIIDNF 1449


RESULT 20
A33996
sodium channel protein I, cardiac - rat
N;Alternate names: sodium channel protein (SkM2) alpha chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33996; JQ0412
R;Rogart, R.B.; Cribbs, L.L.; Muglia, L.K.; Kephart, D.D.; Kaiser, M.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 8170-8174, 1989
A;Title: Molecular cloning of a putative tetrodotoxin-resistant rat heart Na(+) channel
A;Reference number: A33996; MUID:90046760; PMID:2554302
A;Accession: A33996
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2019 <ROG>
A;Cross-references: UNIPROT:P15389; GB:M27902; NID:g206857; PIDN:AAA42114.1; PID:g206858
R;Kallen, R.G.; Sheng, Z.H.; Yang, J.; Chen, L.; Rogart, R.B.; Barchi, R.L.
Neuron 4, 233-242, 1990
A;Title: Primary structure and expression of a sodium channel characteristic of denervat
A;Reference number: JQ0412; MUID:90166613; PMID:2155010
A;Accession: JQ0412
A;Molecule type: mRNA
A;Residues: 1-479,481-1712,'T',1714-1963,'R',1965-2019 <KAL>
A;Experimental source: muscle
C;Superfamily: sodium channel protein
C;Keywords: cardiac muscle; duplication; heart; sodium channel; transmembrane protein

  Query Match             75.0%;  Score 21;  DB 2;  Length 2019;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 FIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||
Db       1455 FIIFGSFFTLNLFIGVIIDNF 1475


RESULT 21
S72458
sodium channel protein para-type alpha chain - house fly (strain Cooper)
C;Species: Musca domestica (house fly)
A;Variety: strain Cooper
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
C;Accession: S72458
R;Williamson, M.S.; Martinez-Torres, D.; Hick, C.A.; Devonshire, A.L.
Mol. Gen. Genet. 252, 51-60, 1996
A;Title: Identification of mutations in the housefly para-type sodium channel gene associ
A;Reference number: S72458; MUID:96397509; PMID:8804403
A;Accession: S72458
A;Molecule type: mRNA
A;Residues: 1-2108 <WIL>
A;Cross-references: UNIPROT:Q94615; EMBL:X96668
A;Experimental source: strain Cooper
C;Genetics:
A;Map position: 3
C;Superfamily: sodium channel protein
C;Keywords: alternative splicing; glycoprotein; phosphoprotein; sodium channel; transmemb
F;302,314,332,967,1451,1470/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;541,1208,1582/Binding site: phosphate (Ser) (covalent) #status predicted

  Query Match             75.0%;  Score 21;  DB 2;  Length 2108;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 FIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||
Db       1531 FIIFGSFFTLNLFIGVIIDNF 1551


RESULT 22
T43161
sodium channel protein TuNaI - sea squirt (Halocynthia roretzi)
C;Species: Halocynthia roretzi
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43161
R;Okamura, Y.; Ono, F.; Okagaki, R.; Chong, J.; Mandel, G.
Neuron 13, 937-948, 1994
A;Title: Neural expression of a sodium channel gene requires cell-specific interactions.
A;Reference number: Z22320; MUID:95033215; PMID:7946338
A;Accession: T43161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2049 <OKA>
A;Cross-references: UNIPROT:Q25150; EMBL:D17311; PIDN:BAA04133.1
C;Superfamily: sodium channel protein
C;Keywords: sodium channel; transmembrane protein

  Query Match             64.3%;  Score 18;  DB 2;  Length 2049;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-10;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 FGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||
```

```
Db       1522 FGSFFTLNLFIGVIIDNF 1539


RESULT 23
A60165
sodium channel protein - fruit fly (Drosophila melanogaster) (fragments)
C;Species: Drosophila melanogaster
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: S04029; A60165
R;Salkoff, L.; Butler, A.; Scavarda, N.; Wei, A.
Nucleic Acids Res. 15, 8569-8572, 1987
A;Title: Nucleotide sequence of the putative sodium channel gene from Drosophila: the fc
A;Reference number: S04029; MUID:88040482; PMID:2444928
A;Accession: S04029
A;Molecule type: DNA
A;Residues: 1-362;363-626;627-1321 <SAL>
A;Cross-references: UNIPROT:Q27930; EMBL:X14394
R;Salkoff, L.; Butler, A.; Wei, A.; Scavarda, N.; Giffen, K.; Ifune, C.; Goodman, R.; Ma
Science 237, 744-749, 1987
A;Title: Genomic organization and deduced amino acid sequence of a putative sodium chann
A;Reference number: A60165; MUID:87292090; PMID:2441469
A;Accession: A60165
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 40-355;363-560,'P',562-626;632-1263 <SA2>
A;Cross-references: EMBL:X14394
A;Note: part of this sequence was confirmed by mRNA sequencing
A;Note: the authors' translation is shown at position 561
C;Genetics:
A;Gene: FlyBase:NaCP60E
A;Cross-references: FlyBase:FBgn0002920
A;Introns: 237/2; 310/3; 362/3; 414/3; 471/3; 531/3; 581/1; 626/3; 751/2; 801/1; 908/1;

  Query Match             60.7%;  Score 17;  DB 2;  Length 1321;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-09;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GSFFTLNLFIGVIIDNF 28
              |||||||||||||||||
Db        886 GSFFTLNLFIGVIIDNF 902


RESULT 24
T31092
probable voltage-gated sodium channel - Aiptasia pallida
C;Species: Aiptasia pallida
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T31092
R;White, G.B.; Pfahnl, A.; Haddock, S.; Lamers, S.; Greenberg, R.M.; Anderson, P.A.V.
submitted to the EMBL Data Library, January 1998
A;Description: Structure of a putative sodium channel from the sea anemone Aiptasia pall
A;Reference number: Z20975
A;Accession: T31092
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1810 <WHI>
A;Cross-references: UNIPROT:O44930; EMBL:AF041851; NID:g2791840; PID:g2791841; PIDN:AAB9
C;Genetics:
A;Gene: Na1
C;Superfamily: sodium channel protein

  Query Match             60.7%;  Score 17;  DB 2;  Length 1810;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-09;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GSFFTLNLFIGVIIDNF 28
              |||||||||||||||||
Db       1294 GSFFTLNLFIGVIIDNF 1310


RESULT 25
CHEE
sodium channel protein - electric eel
C;Species: Electrophorus electricus (electric eel)
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03178; I50536
R;Noda, M.; Shimizu, S.; Tanabe, T.; Takai, T.; Kayano, T.; Ikeda, T.; Takahashi, H.; Nak
da, H.; Miyata, T.; Numa, S.
Nature 312, 121-127, 1984
A;Title: Primary structure of Electrophorus electricus sodium channel deduced from cDNA s
A;Reference number: A03178; MUID:85061498; PMID:6209577
A;Accession: A03178
A;Molecule type: mRNA
A;Residues: 1-1820 <NOD>
A;Cross-references: UNIPROT:P02719; GB:X01119; NID:g62776; PIDN:CAA25587.1; PID:g62777
R;Noda, M.; Numa, S.
J. Recept. Res. 7, 467-497, 1987
A;Title: Structure and function of sodium channel.
A;Reference number: I50536; MUID:87311395; PMID:2442385
A;Accession: I50536
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1820 <NO2>
A;Cross-references: GB:M22252; NID:g1041048; PIDN:AAA79960.1; PID:g1041049
C;Comment: This membrane glycoprotein mediates the voltage-dependent sodium-ion permeabil
ss the membrane, the protein forms a sodium-selective channel through which sodium ions m
C;Comment: This sequence contains four highly homologous internal repeats (excluding resi
 Each repeat has a similar overall structure containing six subregions located in identic
 has a net positive charge (S4), and one is neutral (S2).
C;Comment: The four repeating units are thought to be oriented pseudosymmetrically across
e. The presence of four homologous structures within this molecule is consistent with the
C;Comment: Available data suggest that activation and inactivation gates are located near
955 might, in conjunction with the positively charged residues of S4, act as a voltage se
C;Superfamily: sodium channel protein
C;Keywords: duplication; glycoprotein; ion transport; membrane protein; sodium channel; v
F;111-419,555-807,989-1281,1311-1587/Region: duplication internal repeats I, II, III and
F;111-141,555-585,989-1019,1311-1341/Region: S1 of repeats I through IV
F;150-171,597-620,1033-1057,1353-1376/Region: S2 of repeats I through IV
F;177-197,626-643,1062-1079,1381-1398/Region: S3 of repeats I through IV
F;204-224,651-671,1092-1112,1417-1437/Region: S4 of repeats I through IV
F;244-264,691-711,1132-1152,1454-1474/Region: S5 of repeats I through IV
F;379-402,767-790,1236-1264,1544-1567/Region: S6 of repeats I through IV
F;205,278,288,317,591,690,797,1160,1174,1806/Binding site: carbohydrate (Asn) (covalent)

  Query Match             53.6%;  Score 15;  DB 1;  Length 1820;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 FFTLNLFIGVIIDNF 28
              |||||||||||||||
Db       1253 FFTLNLFIGVIIDNF 1267


Search completed: January 27, 2005, 17:52:46
Job time : 19 secs
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:35:20 ; Search time 92.5 Seconds
(without alignments)
174.167 Million cell updates/sec

Title: US-10-608-584-19
Perfect score: 28
Sequence: 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	100.0	431	2	Q62206	Q62206 mus musculu
2	28	100.0	510	2	Q62242	Q62242 mus musculu
3	28	100.0	742	2	Q90Z29	Q90z29 sternopygus
4	28	100.0	751	2	Q90Z28	Q90z28 sternopygus
5	28	100.0	1136	2	Q804F4	Q804f4 sternopygus
6	28	100.0	1836	1	CIN4_HUMAN	P35499 homo sapien
7	28	100.0	1840	1	CIN4_RAT	P15390 rattus norv
8	28	100.0	1840	2	O70611	O70611 rattus norv
9	28	100.0	1841	2	Q9ER60	Q9er60 mus musculu
10	28	100.0	1951	1	CIN3_RAT	P08104 rattus norv
11	28	100.0	1951	2	Q9C007	Q9c007 homo sapien
12	28	100.0	1981	2	Q8IUJ6	Q8iuj6 homo sapien
13	28	100.0	2000	1	CIN3_HUMAN	Q9ny46 homo sapien
14	28	100.0	2005	1	CIN2_HUMAN	Q99250 homo sapien
15	28	100.0	2005	1	CIN2_RAT	P04775 rattus norv
16	28	100.0	2007	2	Q9YGN7	Q9ygn7 cynops pyrr
17	28	100.0	2009	1	CIN1_HUMAN	P35498 homo sapien
18	28	100.0	2009	1	CIN1_RAT	P04774 rattus norv
19	25	89.3	718	2	Q90Z30	Q90z30 sternopygus
20	25	89.3	743	2	Q90Z26	Q90z26 sternopygus
21	25	89.3	1880	2	Q9IBF1	Q9ibf1 takifugu pa
22	25	89.3	1949	2	Q9DF53	Q9df53 brachydanio
23	25	89.3	1962	2	Q75RX9	Q75rx9 homo sapien
24	25	89.3	1962	2	BAD12085	Bad12085 homo sapi
25	25	89.3	1976	2	Q63541	Q63541 rattus norv
26	25	89.3	1978	1	CIN8_MOUSE	Q9wtu3 mus musculu
27	25	89.3	1978	2	O88420	O88420 rattus norv
28	25	89.3	1980	1	CIN8_HUMAN	Q9uqd0 homo sapien
29	25	89.3	1984	2	Q28644	Q28644 oryctolagus
30	25	89.3	1984	2	O08562	O08562 rattus norv
31	25	89.3	1988	2	O88421	O88421 rattus norv
32	25	89.3	2013	2	Q865W3	Q865w3 canis famil
33	25	89.3	2015	2	Q86UR3	Q86ur3 homo sapien
34	25	89.3	2015	2	Q8IZC9	Q8izc9 homo sapien
35	25	89.3	2015	2	Q96J69	Q96j69 homo sapien
36	25	89.3	2016	1	CIN5_HUMAN	Q14524 homo sapien
37	25	89.3	2016	2	Q75RY0	Q75ry0 homo sapien
38	25	89.3	2016	2	BAD12084	Bad12084 homo sapi
39	25	89.3	2022	2	Q8WMP8	Q8wmp8 bos taurus
40	21	75.0	169	2	Q7PJH1	Q7pjh1 anopheles g
41	21	75.0	210	2	Q9JKC5	Q9jkc5 mus musculu
42	21	75.0	296	2	Q25178	Q25178 heliothis v
43	21	75.0	576	2	Q6DLU1	Q6dlu1 aedes aegyp
44	21	75.0	603	2	Q6DLT6	Q6dlt6 aedes albop
45	21	75.0	626	2	Q6DLT5	Q6dlt5 aedes albop
46	21	75.0	744	2	Q90Z27	Q90z27 sternopygus
47	21	75.0	1130	2	Q9XZC1	Q9xzc1 boophilus m
48	21	75.0	1347	2	Q7PMT4	Q7pmt4 anopheles g
49	21	75.0	1361	2	Q7PJH0	Q7pjh0 anopheles g
50	21	75.0	1444	2	Q9UHM0	Q9uhm0 homo sapien
51	21	75.0	1689	2	Q93135	Q93135 blattella g
52	21	75.0	1695	2	Q94584	Q94584 heliothis v
53	21	75.0	1699	2	O02037	O02037 bdelloura c
54	21	75.0	1717	2	Q90519	Q90519 fugu rubrip
55	21	75.0	1765	2	O88457	O88457 rattus norv
56	21	75.0	1765	2	Q9JMD4	Q9jmd4 mus musculu
57	21	75.0	1765	2	Q9R053	Q9r053 mus musculu
58	21	75.0	1784	2	Q25377	Q25377 loligo opal
59	21	75.0	1791	2	Q8NDX3	Q8ndx3 homo sapien
60	21	75.0	1791	2	Q9UHE0	Q9uhe0 homo sapien
61	21	75.0	1791	2	Q9UI33	Q9ui33 homo sapien
62	21	75.0	1966	2	Q925G6	Q925g6 rattus norv
63	21	75.0	1977	2	Q15858	Q15858 homo sapien
64	21	75.0	2019	1	CIN5_RAT	P15389 rattus norv
65	21	75.0	2019	2	Q9JJV9	Q9jjv9 mus musculu
66	21	75.0	2031	2	O01306	O01306 blattella g
67	21	75.0	2031	2	O01307	O01307 blattella g
68	21	75.0	2051	2	Q86DI7	Q86di7 pediculus h
69	21	75.0	2051	2	Q86DI8	Q86di8 pediculus h
70	21	75.0	2051	2	Q86DI9	Q86di9 pediculus h
71	21	75.0	2058	2	Q6DLT4	Q6dlt4 aedes albop
72	21	75.0	2064	2	Q6DLT3	Q6dlt3 aedes aegyp
73	21	75.0	2086	2	Q86M38	Q86m38 pediculus h
74	21	75.0	2104	2	Q25440	Q25440 musca domes
75	21	75.0	2105	2	Q25439	Q25439 musca domes
76	21	75.0	2108	2	Q94615	Q94615 musca domes
77	21	75.0	2131	1	CINA_DROME	P35500 drosophila
78	18	64.3	2049	2	Q25150	Q25150 halocynthia
79	17	60.7	281	2	Q7JN87	Q7jn87 drosophila
80	17	60.7	297	2	Q6VVE0	Q6vve0 hirudo medi
81	17	60.7	297	2	AAQ81289	Aaq81289 hirudo me
82	17	60.7	1538	2	Q7PF76	Q7pf76 anopheles g
83	17	60.7	1618	2	Q8MMC7	Q8mmc7 drosophila
84	17	60.7	1810	2	O44930	O44930 aiptasia pa
85	17	60.7	2223	2	Q7QIV0	Q7qiv0 anopheles g
86	17	60.7	2304	2	Q9BMQ4	Q9bmq4 blattella g
87	17	60.7	2327	2	Q9W0Y8	Q9w0y8 drosophila
88	16	57.1	1834	2	Q28371	Q28371 equus cabal
89	15	53.6	299	2	Q6VVE1	Q6vve1 hirudo medi
90	15	53.6	299	2	AAQ81288	Aaq81288 hirudo me
91	15	53.6	301	2	Q6VVE2	Q6vve2 hirudo medi
92	15	53.6	301	2	AAQ81287	Aaq81287 hirudo me
93	15	53.6	1089	2	Q8IS97	Q8is97 varroa dest
94	15	53.6	1820	1	CINA_ELEEL	P02719 electrophor
95	15	53.6	2215	2	Q86D77	Q86d77 varroa dest
96	13	46.4	1993	2	P90670	P90670 aplysia cal
97	12	42.9	717	2	Q90Z25	Q90z25 sternopygus
98	12	42.9	1695	2	O62604	O62604 polyorchis
99	12	42.9	1740	2	Q17314	Q17314 cyanea capi
100	12	42.9	1956	2	Q9Y5Y9	Q9y5y9 homo sapien

ALIGNMENTS

```
RESULT 1
Q62206
ID   Q62206      PRELIMINARY;      PRT;   431 AA.
AC   Q62206;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel 3.
GN   Name=Scn1a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Jover E., Shah V.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; L42339; AAA67107.1; -.
DR   HSSP; P04775; 1BYY.
DR   MGD; MGI:98246; Scn1a.
DR   GO; GO:0005624; C:membrane fraction; IDA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
SQ   SEQUENCE   431 AA;  49466 MW;  9CD841FF73D1D9B7 CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db        357 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 384


RESULT 2
Q62242
ID   Q62242      PRELIMINARY;      PRT;   510 AA.
AC   Q62242;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Jover E., Shah V.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; L42341; AAA67695.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF00612; IQ; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
FT   NON_TER     510    510
SQ   SEQUENCE   510 AA;  58397 MW;  02DCC7DAED3796E8 CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 510;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28


RESULT 3
Q90Z29
ID   Q90Z29      PRELIMINARY;      PRT;   742 AA.
AC   Q90Z29;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel 2 (Fragment).
OS   Sternopygus macrurus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC   Sternopygidae; Sternopygus.
OX   NCBI_TaxID=77841;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21310016; PubMed=11416226;
RA   Lopreato G.F., Lu Y., Southwell A., Atkinson N.S., Hillis D.M.,
RA   Wilcox T.P., Zakon H.H.;
RT   "Evolution and divergence of sodium channel genes in vertebrates.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7588-7592(2001).
DR   EMBL; AF378140; AAK55438.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 2.
DR   Pfam; PF06512; Na_trans_assoc; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1      1
FT   NON_TER     742    742
SQ   SEQUENCE   742 AA;  84353 MW;  7F4B30038D3F2AC4 CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 742;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db        641 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 668


RESULT 4
Q90Z28
ID   Q90Z28      PRELIMINARY;      PRT;   751 AA.
AC   Q90Z28;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel 3 (Fragment).
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OS   Sternopygus macrurus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC   Sternopygidae; Sternopygus.
OX   NCBI_TaxID=77841;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21310016; PubMed=11416226;
RA   Lopreato G.F., Lu Y., Southwell A., Atkinson N.S., Hillis D.M.,
RA   Wilcox T.P., Zakon H.H.;
RT   "Evolution and divergence of sodium channel genes in vertebrates.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7588-7592(2001).
DR   EMBL; AF378141; AAK55439.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 2.
DR   Pfam; PF06512; Na_trans_assoc; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1      1
FT   NON_TER     751    751
SQ   SEQUENCE   751 AA;  84598 MW;  CBFE6162E90A76FC CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 751;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db        674 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 701


RESULT 5
Q804F4
ID   Q804F4      PRELIMINARY;      PRT;  1136 AA.
AC   Q804F4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel 7 (Fragment).
GN   Name=Na7;
OS   Sternopygus macrurus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC   Sternopygidae; Sternopygus.
OX   NCBI_TaxID=77841;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lu Y., Lopreato G.F., Zakon H.H.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
DR   EMBL; AY183895; AAO23570.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005891; C:voltage-gated calcium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.
DR   GO; GO:0006816; P:calcium ion transport; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 3.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00167; CACHANNEL.
KW   Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KW   Transmembrane; Transport; Voltage-gated channel.
FT   NON_TER       1      1
FT   NON_TER    1136   1136
SQ   SEQUENCE   1136 AA;  129141 MW;  ECDE52D025B50664 CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 1136;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1042 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1069


RESULT 6
CIN4_HUMAN
ID   CIN4_HUMAN     STANDARD;      PRT;  1836 AA.
AC   P35499; Q15478; Q16447; Q7Z6B1;
DT   01-JUN-1994 (Rel. 29, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type IV alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.4) (Sodium channel protein, skeletal muscle
DE   alpha-subunit).
GN   Name=SCN4A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANT ASP-559.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=92246457; PubMed=1315496;
RA   George A.L. Jr., Komisarof J., Kallen R.G., Barchi R.L.;
RT   "Primary structure of the adult human skeletal muscle voltage-
RT   dependent sodium channel.";
RL   Ann. Neurol. 31:131-137(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92134303; PubMed=1310396;
RA   Wang J., Rojas C.V., Zhou J., Schwartz L.S., Nicholas H.,
RA   Hoffmann E.P.;
RT   "Sequence and genomic structure of the human adult skeletal muscle
RT   sodium channel alpha subunit gene on 17q.";
RL   Biochem. Biophys. Res. Commun. 182:794-801(1992).
RN   [3]
RP   SEQUENCE FROM N.A., VARIANT MYASTHENIC SYNDROME GLU-1442, AND VARIANTS
RP   LEU-246; ASP-559 AND ASN-1376.
RX   MEDLINE=22684480; PubMed=12766226; DOI=10.1073/pnas.1230273100;
RA   Tsujino A., Maertens C., Ohno K., Shen X.-M., Fukuda T., Harper C.M.,
RA   Cannon S.C., Engel A.G.;
RT   "Myasthenic syndrome caused by mutation of the SCN4A sodium channel.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:7377-7382(2003).
RN   [4]
RP   SEQUENCE FROM N.A., AND VARIANT ASN-1376.
RX   MEDLINE=93338444; PubMed=1339144;
RA   McClatchey A.I., Lin C.S., Wang J., Hoffman E.P., Rojas C.V.,
RA   Gusella J.F.;
RT   "The genomic structure of the human skeletal muscle sodium channel
RT   gene.";
RL   Hum. Mol. Genet. 1:521-521(1992).
RN   [5]
RP   SEQUENCE OF 1305-1339 FROM N.A., AND VARIANTS PMC VAL-1306 AND
RP   MET-1313.
RX   MEDLINE=92154689; PubMed=1310898;
RA   McClatchey A.I., van den Bergh P., Pericak-Vance M.A., Raskind W.,
RA   Verellen C., McKenna-Yasek D., Rao K., Haines J.L., Bird T.,
RA   Brown R.H. Jr., Gusella J.F.;
RT   "Temperature-sensitive mutations in the III-IV cytoplasmic loop region
RT   of the skeletal muscle sodium channel gene in paramyotonia
RT   congenita.";
```

RL Cell 68:769-774(1992).
RN [6]
RP VARIANT HYPP MET-704.
RX MEDLINE=92069747; PubMed=1659948;
RA Ptacek L.J., George A.L. Jr., Griggs R.C., Tawil R., Kallen R.G.,
RA Barchi R.L., Robertson M., Leppert M.F.;
RT "Identification of a mutation in the gene causing hyperkalemic
RT periodic paralysis.";
RL Cell 67:1021-1027(1991).
RN [7]
RP VARIANT HYPP VAL-1592.
RX MEDLINE=92065978; PubMed=1659668;
RA Rojas C.V., Wang J., Schwartz L.S., Hoffman E.P., Powell B.R.,
RA Brown R.H. Jr.;
RT "A Met-to-Val mutation in the skeletal muscle Na+ channel alpha-
RT subunit in hyperkalaemic periodic paralysis.";
RL Nature 354:387-389(1991).
RN [8]
RP VARIANTS PMC PHE-804 AND THR-1156.
RX MEDLINE=93265141; PubMed=1338909;
RA McClatchey A.I., McKenna-Yasek D., Cros D., Worthen H.G., Kuncl R.W.,
RA Desilva S.M., Cornblath D.R., Gusella J.F., Brown R.H. Jr.;
RT "Novel mutations in families with unusual and variable disorders of
RT the skeletal muscle sodium channel.";
RL Nat. Genet. 2:148-152(1992).
RN [9]
RP VARIANTS PMC CYS-1448 AND HIS-1448.
RX MEDLINE=92265302; PubMed=1316765;
RA Ptacek L.J., George A.L. Jr., Barchi R.L., Griggs R.C., Riggs J.E.,
RA Robertson M., Leppert M.F.;
RT "Mutations in an S4 segment of the adult skeletal muscle sodium
RT channel cause paramyotonia congenita.";
RL Neuron 8:891-897(1992).
RN [10]
RP VARIANT PMC ARG-1433.
RX MEDLINE=93270429; PubMed=8388676;
RA Ptacek L.J., Gouw L., Kwiecinski H., McManis P., Mendell J.R.,
RA Barohn R.J., George A.L. Jr., Barchi R.L., Robertson M., Leppert M.F.;
RT "Sodium channel mutations in paramyotonia congenita and hyperkalemic
RT periodic paralysis.";
RL Ann. Neurol. 33:300-307(1993).
RN [11]
RP VARIANTS PMC ALA-1306; GLU-1306 AND VAL-1306.
RX MEDLINE=94141728; PubMed=8308722;
RA Lerche H., Heine R., Pika U., George A.L. Jr., Mitrovic N.,
RA Browatzki M., Weiss T., Rivet-Bastide M., Franke C., Lomonaco M.,
RA Ricker K., Lehmann-Horn F.;
RT "Human sodium channel myotonia: slowed channel inactivation due to
RT substitutions for a glycine within the III-IV linker.";
RL J. Physiol. (Lond.) 470:13-22(1993).
RN [12]
RP VARIANT PMC MET-1589.
RX MEDLINE=94061027; PubMed=8242056;
RA Heine R., Pika U., Lehmann-Horn F.;
RT "A novel SCN4A mutation causing myotonia aggravated by cold and
RT potassium.";
RL Hum. Mol. Genet. 2:1349-1353(1993).
RN [13]
RP VARIANT POTASSIUM-AGGRAVATED MYOTONIA VAL-1160.
RX PubMed=8058156;
RA Ptacek L.J., Tawil R., Griggs R.C., Meola G., McManis P., Barohn R.J.,
RA Mendell J.R., Harris C., Spitzer R., Santiago F., Leppert M.F.;
RT "Sodium channel mutations in acetazolamide-responsive myotonia
RT congenita, paramyotonia congenita, and hyperkalemic periodic
RT paralysis.";
RL Neurology 44:1500-1503(1994).
RN [14]
RP VARIANT PARAMYOTONIA WITHOUT COLD PARALYSIS ILE-1293.
RX MEDLINE=96154961; PubMed=8580427;
RA Koch M.C., Baumbach K., George A.L., Ricker K.;
RT "Paramyotonia congenita without paralysis on exposure to cold: a novel
RT mutation in the SCN4A gene (Val1293Ile).";
RL NeuroReport 6:2001-2004(1995).
RN [15]
RP VARIANT POTASSIUM-AGGRAVATED MYOTONIA MET-445.
RX PubMed=9392583;
RA Rosenfeld J., Sloan-Brown K., George A.L. Jr.;
RT "A novel muscle sodium channel mutation causes painful congenital
RT myotonia.";
RL Ann. Neurol. 42:811-814(1997).
RN [16]
RP VARIANT POTASSIUM-AGGRAVATED MYOTONIA MET-445.
RX PubMed=10218481;
RA Wang D.W., VanDeCarr D., Ruben P.C., George A.L. Jr., Bennett P.B.;
RT "Functional consequences of a domain 1/S6 segment sodium channel
RT mutation associated with painful congenital myotonia.";
RL FEBS Lett. 448:231-234(1999).
RN [17]
RP VARIANT HYPOKPP HIS-669.
RX PubMed=10599760;
RA Bulman D.E., Scoggan K.A., van Oene M.D., Nicolle M.W., Hahn A.F.,
RA Tollar L.L., Ebers G.C.;
RT "A novel sodium channel mutation in a family with hypokalemic periodic
RT paralysis.";
RL Neurology 53:1932-1936(1999).
RN [18]
RP VARIANT HYPOKPP SER-1158.
RX PubMed=10851391;
RA Sugiura Y., Aoki T., Sugiyama Y., Hida C., Ogata M., Yamamoto T.;
RT "Temperature-sensitive sodium channelopathy with heat-induced myotonia
RT and cold-induced paralysis.";
RL Neurology 54:2179-2181(2000).
RN [19]
RP VARIANTS HYPOKPP GLY-672 AND HIS-672.
RX PubMed=10944223;
RA Jurkat-Rott K., Mitrovic N., Hang C., Kouzmekine A., Iaizzo P.,
RA Herzog J., Lerche H., Nicole S., Vale-Santos J., Chauveau D.,
RA Fontaine B., Lehmann-Horn F.;
RT "Voltage-sensor sodium channel mutations cause hypokalemic periodic
RT paralysis type 2 by enhanced inactivation and reduced current.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9549-9554(2000).
RN [20]
RP VARIANT HYPOKPP SER-672.
RX PubMed=11558801;
RA Bendahhou S., Cummins T.R., Griggs R.C., Fu Y.H., Ptacek L.J.;
RT "Sodium channel inactivation defects are associated with
RT acetazolamide-exacerbated hypokalemic periodic paralysis.";
RL Ann. Neurol. 50:417-420(2001).
RN [21]
RP VARIANT HYPOKPP SER-672.
RX PubMed=11591859;
RA Davies N.P., Eunson L.H., Samuel M., Hanna M.G.;
RT "Sodium channel gene mutations in hypokalemic periodic paralysis: an
RT uncommon cause in the UK.";
RL Neurology 57:1323-1325(2001).
CC -!- FUNCTION: This protein mediates the voltage-dependent sodium ion
CC permeability of excitable membranes. Assuming opened or closed
CC conformations in response to the voltage difference across the
CC membrane, the protein forms a sodium-selective channel through
CC which Na+ ions may pass in accordance with their electrochemical
CC gradient. This sodium channel may be present in both denervated
CC and innervated skeletal muscle.
CC -!- SUBUNIT: Muscle sodium channels contain an alpha subunit and a
CC smaller beta subunit. Interacts with the PDZ domain of the
CC syntrophin SNTA1, SNTB1 and SNTB2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC segment (S4). Segments S4 are probably the voltage-sensors and are
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -!- DISEASE: Defects in SCN4A are the cause of paramyotonia congenita
CC of von Eulenburg (PMC) [MIM:168300]. PMC is an autosomal dominant
CC sodium channel disease characterized by myotonia, increased by
CC exposure to cold, intermittent flaccid paresis, not necessarily

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  Query Match           100.0%;  Score 28;  DB 1;  Length 1836;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1271 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1298


RESULT 7
CIN4_RAT
ID   CIN4_RAT       STANDARD;      PRT;  1840 AA.
AC   P15390;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type IV alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.4) (Sodium channel protein, skeletal muscle
DE   alpha-subunit) (Mu-1).
GN   Name=Scn4a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90148778; PubMed=2559760;
RA   Trimmer J.S., Cooperman S.S., Tomiko S.A., Zhou J., Crean S.M.,
RA   Boyle M.B., Kallen R.G., Sheng Z., Barchi R.L., Sigworth F.J.,
RA   Goodman R.H., Agnew W.S., Mandel G.;
RT   "Primary structure and functional expression of a mammalian skeletal
RT   muscle sodium channel.";
RL   Neuron 3:33-49(1989).
CC   -!- FUNCTION: This protein mediates the voltage-dependent sodium ion
CC       permeability of excitable membranes. Assuming opened or closed
CC       conformations in response to the voltage difference across the
CC       membrane, the protein forms a sodium-selective channel through
CC       which Na+ ions may pass in accordance with their electrochemical
CC       gradient. This sodium channel may be present in both denervated
CC       and innervated skeletal muscle.
CC   -!- SUBUNIT: Muscle sodium channels contain an alpha subunit and a
CC       smaller beta subunit. Interacts with the PDZ domain of the
CC       syntrophin SNTA1, SNTB1 and SNTB2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M26643; AAA41682.1; -.
DR   PIR; JN0007; CHRTM1.
DR   HSSP; P04775; 1BYY.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008052; Na_channel4.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01665; NACHANNEL4.
DR   PROSITE; PS50096; IQ; 1.
KW   Glycoprotein; Ion transport; Ionic channel; Multigene family;
KW   Phosphorylation; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   TRANSMEM    130    152       S1 of repeat I.
FT   TRANSMEM    156    179       S2 of repeat I.
FT   TRANSMEM    192    212       S3 of repeat I.
FT   TRANSMEM    214    233       S4 of repeat I.
FT   TRANSMEM    252    274       S5 of repeat I.
FT   TRANSMEM    417    444       S6 of repeat I.
FT   TRANSMEM    571    593       S1 of repeat II.
FT   TRANSMEM    663    685       S2 of repeat II.
FT   TRANSMEM    696    721       S3 of repeat II.
FT   TRANSMEM    722    737       S4 of repeat II.
FT   TRANSMEM    756    778       S5 of repeat II.
FT   TRANSMEM    832    859       S6 of repeat II.
FT   TRANSMEM   1084   1105       S1 of repeat III.
FT   TRANSMEM   1117   1140       S2 of repeat III.
FT   TRANSMEM   1149   1168       S3 of repeat III.
FT   TRANSMEM   1176   1195       S4 of repeat III.
FT   TRANSMEM   1215   1236       S5 of repeat III.
FT   TRANSMEM   1324   1351       S6 of repeat III.
FT   TRANSMEM   1405   1427       S1 of repeat IV.
FT   TRANSMEM   1437   1460       S2 of repeat IV.
FT   TRANSMEM   1468   1487       S3 of repeat IV.
FT   TRANSMEM   1502   1522       S4 of repeat IV.
FT   TRANSMEM   1535   1556       S5 of repeat IV.
FT   TRANSMEM   1627   1653       S6 of repeat IV.
FT   DOMAIN     1720   1749       IQ.
FT   CARBOHYD    288    288       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    291    291       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    297    297       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    303    303       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    309    309       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    315    315       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    327    327       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    356    356       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    502    502       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    954    954       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1198   1198       N-linked (GlcNAc. . .) (Potential).
FT   MOD_RES      56     56       Phosphoserine (by PKA) (Potential).
FT   MOD_RES     251    251       Phosphoserine (by PKA) (Potential).
FT   MOD_RES    1321   1321       Phosphoserine (by PKA) (Potential).
FT   MOD_RES    1504   1504       Phosphoserine (by PKA) (Potential).
SQ   SEQUENCE   1840 AA;  208865 MW;  C5DC09D93DD9FAD6 CRC64;

  Query Match           100.0%;  Score 28;  DB 1;  Length 1840;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1264 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1291


RESULT 8
O70611
ID   O70611       PRELIMINARY;      PRT;  1840 AA.
AC   O70611;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Rat skeletal muscle type 1 voltage-gated sodium channel (RSkM1)
DE   variant.
GN   Name=SCN4A;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
```

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RP   SEQUENCE FROM N.A.
RC   STRAIN=Copenhagen; TISSUE=Prostate;
RX   MEDLINE=98273645; PubMed=9613589;
RA   Diss J.K.J., Stewart D., Fraser S.P., Black J.A., Dibb-Hajj S.,
RA   Waxman S.G., Archer S.N., Djamgoz M.B.A.;
RT   "Expression of skeletal muscle-type voltage-gated Na+ channel in rat
RT   and human prostate cancer cell lines.";
RL   FEBS Lett. 427:5-10(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; Y17153; CAA76659.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008052; Na_channel4.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01665; NACHANNEL4.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1840 AA;  208823 MW;  B1DFFA538E264B40 CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 1840;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1264 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1291


RESULT 9
Q9ER60
ID   Q9ER60      PRELIMINARY;      PRT;  1841 AA.
AC   Q9ER60;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel.
GN   Name=Scn4a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=balb/c; TISSUE=Heart;
RX   MEDLINE=21823196; PubMed=11834499;
RA   Zimmer T., Benndorf K.;
RT   "The mouse heart sodium channel (mH1): cloning and characterization of
RT   alternatively spliced variants.";
RL   Am. J. Physiol. Heart Circ. Physiol. 282:H1007-H1017(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AJ278787; CAC17146.1; -.
DR   HSSP; P04775; 1BYY.
DR   MGD; MGI:98250; Scn4a.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008052; Na_channel4.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01665; NACHANNEL4.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1841 AA;  208796 MW;  0766DFD33A9E0E55 CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 1841;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1265 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1292


RESULT 10
CIN3_RAT
ID   CIN3_RAT       STANDARD;      PRT;  1951 AA.
AC   P08104;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Sodium channel protein type III alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.3) (Sodium channel protein, brain III alpha
DE   subunit) (Voltage-gated sodium channel subtype III).
GN   Name=Scn3a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar;
RX   MEDLINE=88137594; PubMed=2449363;
RA   Kayano T., Noda M., Flockerzi V., Takahashi H., Numa S.;
RT   "Primary structure of rat brain sodium channel III deduced from the
RT   cDNA sequence.";
RL   FEBS Lett. 228:187-194(1988).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y00766; CAA68735.1; -.
DR   PIR; S00320; S00320.
DR   PDB; 1QG9; NMR; A=156-176.
DR   RGD; 3635; Scn3a.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; FALSE_NEG.
KW   3D-structure; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   REPEAT      110    455       I.
FT   REPEAT      693    965       II.
FT   REPEAT     1139   1450       III.
FT   REPEAT     1459   1757       IV.
FT   TRANSMEM    124    147       S1 of repeat I.
FT   TRANSMEM    156    175       S2 of repeat I.
FT   TRANSMEM    189    207       S3 of repeat I.
FT   TRANSMEM    214    233       S4 of repeat I.
FT   TRANSMEM    249    273       S5 of repeat I.
FT   TRANSMEM    401    426       S6 of repeat I.
FT   TRANSMEM    706    730       S1 of repeat II.
FT   TRANSMEM    742    765       S2 of repeat II.
FT   TRANSMEM    774    793       S3 of repeat II.
FT   TRANSMEM    800    820       S4 of repeat II.
FT   TRANSMEM    836    856       S5 of repeat II.
FT   TRANSMEM    910    935       S6 of repeat II.
FT   TRANSMEM   1153   1176       S1 of repeat III.
FT   TRANSMEM   1190   1215       S2 of repeat III.
FT   TRANSMEM   1222   1243       S3 of repeat III.
FT   TRANSMEM   1248   1269       S4 of repeat III.
FT   TRANSMEM   1289   1310       S5 of repeat III.
FT   TRANSMEM   1393   1419       S6 of repeat III.
FT   TRANSMEM   1473   1496       S1 of repeat IV.
FT   TRANSMEM   1508   1531       S2 of repeat IV.
FT   TRANSMEM   1538   1561       S3 of repeat IV.
FT   TRANSMEM   1572   1593       S4 of repeat IV.
FT   TRANSMEM   1609   1631       S5 of repeat IV.
FT   TRANSMEM   1698   1722       S6 of repeat IV.
FT   CARBOHYD    211    211       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    290    290       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    296    296       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    302    302       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    307    307       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    339    339       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    624    624       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    835    835       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1002   1002       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1019   1019       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1085   1085       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1317   1317       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1331   1331       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   1951 AA;  221385 MW;  74E5E851524BD10E CRC64;

  Query Match           100.0%;  Score 28;  DB 1;  Length 1951;
  Best Local Similarity  100.0%;  Pred. No. 5.4e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1395 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1422


RESULT 11
Q9C007
ID   Q9C007      PRELIMINARY;      PRT;  1951 AA.
AC   Q9C007;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel alpha subunit splice variant SCN3A-
DE   s.
GN   Name=SCN3A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jeong S.-Y., Goto J., Kanazawa I.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AF225986; AAK00218.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1951 AA;  221517 MW;  99AD4C032CE124AB CRC64;

  Query Match           100.0%;  Score 28;  DB 2;  Length 1951;
  Best Local Similarity  100.0%;  Pred. No. 5.4e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1395 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1422


RESULT 12
Q8IUJ6
ID   Q8IUJ6      PRELIMINARY;      PRT;  1981 AA.
AC   Q8IUJ6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel alpha 1 subunit.
GN   Name=SCN1A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
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RP   SEQUENCE FROM N.A.
RC   TISSUE=Normal brain;
RA   Ouchida M., Ohmori I.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AB098335; BAC45228.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008051; Na_channel1.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   InterPro; IPR000100; Ribonuclease_P.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01664; NACHANNEL1.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS00648; RIBONUCLEASE_P; UNKNOWN_1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1981 AA;  226201 MW;  B1D6946D6491B7AD CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 1981;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1431 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1458


RESULT 13
CIN3_HUMAN
ID   CIN3_HUMAN     STANDARD;      PRT;  2000 AA.
AC   Q9NY46; Q16142; Q9BZB3; Q9C006; Q9NYK2; Q9UPD1; Q9Y6P4;
DT   16-OCT-2001 (Rel. 40, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Sodium channel protein type III alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.3) (Sodium channel protein, brain III alpha
DE   subunit) (Voltage-gated sodium channel subtype III).
GN   Name=SCN3A; Synonyms=NAC3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Brain;
RA   Chen Y., Dale T.J., Romanos M.A., Whitaker W.R., Xie X., Clare J.J.;
RT   "Cloning, distribution and functional analysis of the human brain type
RT   III sodium channel from human brain.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RA   Jeong S.-Y., Goto J., Kanazawa I.;
RT   "Cloning of cDNA for human voltage-gated sodium channel alpha subunit,
RT   SCN3A.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND VARIANT THR-606.
RX   MEDLINE=21142400; PubMed=11245985; DOI=10.1016/S0378-1119(00)00594-1;
RA   Kasai N., Fukushima K., Ueki Y., Prasad S., Nosakowski J.,
RA   Sugata K.-I., Sugata A., Nishizaki K., Meyer N.C., Smith R.J.H.;
RT   "Genomic structures of SCN2A and SCN3A - candidate genes for deafness
RT   at the DFNA16 locus.";
RL   Gene 264:113-122(2001).
RN   [4]
RP   SEQUENCE OF 1-1415 FROM N.A. (ISOFORMS 2 AND 4).
RC   TISSUE=Brain;
RX   MEDLINE=98251277; PubMed=9589372;
RA   Lu C.M., Brown G.B.;
RT   "Isolation of a human-brain sodium-channel gene encoding two isoforms
RT   of the subtype III alpha-subunit.";
RL   J. Mol. Neurosci. 10:67-70(1998).
RN   [5]
RP   SEQUENCE OF 1324-1413 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=94211784; PubMed=8159690;
RA   Malo M.S., Srivastava K., Andresen J.M., Chen X.N., Korenberg J.R.,
RA   Ingram V.M.;
RT   "Targeted gene walking by low stringency polymerase chain reaction:
RT   assignment of a putative human brain sodium channel gene (SCN3A) to
RT   chromosome 2q24-31.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:2975-2979(1994).
RN   [6]
RP   SEQUENCE OF 1669-1750 FROM N.A.
RC   TISSUE=Kidney;
RA   Tonkovich G.S., Kyle J.W.;
RT   "Endogenous sodium current in HEK293 cells: increase in cell surface
RT   expression of endogenous currents by stable transfection of the Beta 1
RT   subunit.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC         Comment=Exons 6A and 6N only differ by a single residue;
CC       Name=1; Synonyms=6A-12+12b;
CC         IsoId=Q9NY46-1; Sequence=Displayed;
CC       Name=2; Synonyms=6A-12;
CC         IsoId=Q9NY46-2; Sequence=VSP_001034;
CC       Name=3; Synonyms=6N-12+12b;
CC         IsoId=Q9NY46-3; Sequence=VSP_001033;
CC       Name=4; Synonyms=6N-12;
CC         IsoId=Q9NY46-4; Sequence=VSP_001033, VSP_001034;
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ251507; CAB85895.1; -.
DR   EMBL; AF225987; AAK00219.1; -.
DR   EMBL; AF330135; AAG53414.1; -.
DR   EMBL; AF330118; AAG53414.1; JOINED.
DR   EMBL; AF330119; AAG53414.1; JOINED.
DR   EMBL; AF330120; AAG53414.1; JOINED.
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DR   EMBL; AF330121; AAG53414.1; JOINED.
DR   EMBL; AF330122; AAG53414.1; JOINED.
DR   EMBL; AF330123; AAG53414.1; JOINED.
DR   EMBL; AF330124; AAG53414.1; JOINED.
DR   EMBL; AF330125; AAG53414.1; JOINED.
DR   EMBL; AF330126; AAG53414.1; JOINED.
DR   EMBL; AF330127; AAG53414.1; JOINED.
DR   EMBL; AF330128; AAG53414.1; JOINED.
DR   EMBL; AF330129; AAG53414.1; JOINED.
DR   EMBL; AF330130; AAG53414.1; JOINED.
DR   EMBL; AF330131; AAG53414.1; JOINED.
DR   EMBL; AF330132; AAG53414.1; JOINED.
DR   EMBL; AF330133; AAG53414.1; JOINED.
DR   EMBL; AF330134; AAG53414.1; JOINED.
DR   EMBL; AF330135; AAG53415.1; -.
DR   EMBL; AF330118; AAG53415.1; JOINED.
DR   EMBL; AF330119; AAG53415.1; JOINED.
DR   EMBL; AF330120; AAG53415.1; JOINED.
DR   EMBL; AF330121; AAG53415.1; JOINED.
DR   EMBL; AF330122; AAG53415.1; JOINED.
DR   EMBL; AF330123; AAG53415.1; JOINED.
DR   EMBL; AF330124; AAG53415.1; JOINED.
DR   EMBL; AF330125; AAG53415.1; JOINED.
DR   EMBL; AF330126; AAG53415.1; JOINED.
DR   EMBL; AF330127; AAG53415.1; JOINED.
DR   EMBL; AF330128; AAG53415.1; JOINED.
DR   EMBL; AF330129; AAG53415.1; JOINED.
DR   EMBL; AF330130; AAG53415.1; JOINED.
DR   EMBL; AF330131; AAG53415.1; JOINED.
DR   EMBL; AF330132; AAG53415.1; JOINED.
DR   EMBL; AF330133; AAG53415.1; JOINED.
DR   EMBL; AF330134; AAG53415.1; JOINED.
DR   EMBL; AF035685; AAC29514.1; -.
DR   EMBL; AF035686; AAC29515.1; -.
DR   EMBL; S69887; AAB30530.1; -.
DR   EMBL; AF239921; AAF44690.1; -.
DR   PIR; A54937; A54937.
DR   HSSP; P04775; 1BYY.
DR   Genew; HGNC:10590; SCN3A.
DR   MIM; 182391; -.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; NAS.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; NAS.
DR   GO; GO:0006814; P:sodium ion transport; NAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Polymorphism; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   TRANSMEM    124    147       S1 of repeat I.
FT   TRANSMEM    156    175       S2 of repeat I.
FT   TRANSMEM    189    207       S3 of repeat I.
FT   TRANSMEM    214    233       S4 of repeat I.
FT   TRANSMEM    249    273       S5 of repeat I.
FT   TRANSMEM    401    426       S6 of repeat I.
FT   TRANSMEM    755    779       S1 of repeat II.
FT   TRANSMEM    791    814       S2 of repeat II.
FT   TRANSMEM    823    842       S3 of repeat II.
FT   TRANSMEM    849    869       S4 of repeat II.
FT   TRANSMEM    885    905       S5 of repeat II.
FT   TRANSMEM    959    984       S6 of repeat II.
FT   TRANSMEM   1202   1225       S1 of repeat III.
FT   TRANSMEM   1239   1264       S2 of repeat III.
FT   TRANSMEM   1271   1292       S3 of repeat III.
FT   TRANSMEM   1297   1318       S4 of repeat III.
FT   TRANSMEM   1338   1359       S5 of repeat III.
FT   TRANSMEM   1442   1468       S6 of repeat III.
FT   TRANSMEM   1522   1545       S1 of repeat IV.
FT   TRANSMEM   1557   1580       S2 of repeat IV.
FT   TRANSMEM   1587   1610       S3 of repeat IV.
FT   TRANSMEM   1621   1642       S4 of repeat IV.
FT   TRANSMEM   1658   1680       S5 of repeat IV.
FT   TRANSMEM   1747   1771       S6 of repeat IV.
FT   DOMAIN     1900   1929       IQ.
FT   CARBOHYD    211    211       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    290    290       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    296    296       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    302    302       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    307    307       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    339    339       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    624    624       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    884    884       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1051   1051       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1068   1068       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1134   1134       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1366   1366       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1380   1380       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    208    208       S -> D (in isoform 3 and isoform 4).
FT                                /FTId=VSP_001033.
FT   VARSPLIC    625    673       Missing (in isoform 2 and isoform 4).

  Query Match             100.0%;  Score 28;  DB 1;  Length 2000;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1444 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1471


RESULT 14
CIN2_HUMAN
ID   CIN2_HUMAN     STANDARD;      PRT;  2005 AA.
AC   Q99250; Q14472; Q9BZC9; Q9BZD0;
DT   01-JUN-1994 (Rel. 29, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type II alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha
DE   subunit) (HBSC II).
GN   Name=SCN2A; Synonyms=SCN2A2, NAC2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=92390418; PubMed=1325650;
RA   Ahmed C.M., Ware D.H., Lee S.C., Patten C.D., Ferrer-Montiel A.V.,
RA   Schinder A.F., McPherson J.D., Wagner-Mcpherson C.B., Wasmuth J.J.,
RA   Evans G.A., Montal M.;
RT   "Primary structure, chromosomal localization, and functional
RT   expression of a voltage-gated sodium channel from human brain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:8220-8224(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX   MEDLINE=21142400; PubMed=11245985; DOI=10.1016/S0378-1119(00)00594-1;
RA   Kasai N., Fukushima K., Ueki Y., Prasad S., Nosakowski J.,
RA   Sugata K.-I., Sugata A., Nishizaki K., Meyer N.C., Smith R.J.H.;
RT   "Genomic structures of SCN2A and SCN3A - candidate genes for deafness
RT   at the DFNA16 locus.";
RL   Gene 264:113-122(2001).
RN   [3]
RP   SEQUENCE OF 1-89 FROM N.A.
RA   Lu C.-M., Eichelberger J.S., Beckman M.L., Schade S.D., Brown G.B.;
RT   "Isolation of the 5'-flanking region for human brain sodium channel
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RT   subtype II alpha-Subunit (SCN2A).";
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1702-2005 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92275082; PubMed=1317301;
RA   Lu C.-M., Han J., Rado T.A., Brown G.B.;
RT   "Differential expression of two sodium channel subtypes in human
RT   brain.";
RL   FEBS Lett. 303:53-58(1992).
RN   [5]
RP   SEQUENCE OF 1702-1772 FROM N.A.
RX   MEDLINE=91110524; PubMed=1846440;
RA   Han J., Lu C.-M., Brown G.B., Rado T.A.;
RT   "Direct amplification of a single dissected chromosomal segment by
RT   polymerase chain reaction: a human brain sodium channel gene is on
RT   chromosome 2q22-q23.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:335-339(1991).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Adult, 6A;
CC         IsoId=Q99250-1; Sequence=Displayed;
CC       Name=2; Synonyms=Neonatal, 6N;
CC         IsoId=Q99250-2; Sequence=VSP_001032;
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M94055; AAA18895.1; -.
DR   EMBL; AF059683; AAC14574.1; -.
DR   EMBL; AF327246; AAG53413.1; -.
DR   EMBL; AF327226; AAG53413.1; JOINED.
DR   EMBL; AF327227; AAG53413.1; JOINED.
DR   EMBL; AF327228; AAG53413.1; JOINED.
DR   EMBL; AF327229; AAG53413.1; JOINED.
DR   EMBL; AF327230; AAG53413.1; JOINED.
DR   EMBL; AF327231; AAG53413.1; JOINED.
DR   EMBL; AF327232; AAG53413.1; JOINED.
DR   EMBL; AF327233; AAG53413.1; JOINED.
DR   EMBL; AF327234; AAG53413.1; JOINED.
DR   EMBL; AF327235; AAG53413.1; JOINED.
DR   EMBL; AF327236; AAG53413.1; JOINED.
DR   EMBL; AF327237; AAG53413.1; JOINED.
DR   EMBL; AF327238; AAG53413.1; JOINED.
DR   EMBL; AF327239; AAG53413.1; JOINED.
DR   EMBL; AF327240; AAG53413.1; JOINED.
DR   EMBL; AF327241; AAG53413.1; JOINED.
DR   EMBL; AF327242; AAG53413.1; JOINED.
DR   EMBL; AF327243; AAG53413.1; JOINED.
DR   EMBL; AF327244; AAG53413.1; JOINED.
DR   EMBL; AF327245; AAG53413.1; JOINED.
DR   EMBL; AF327246; AAG53412.1; -.
DR   EMBL; AF327226; AAG53412.1; JOINED.
DR   EMBL; AF327227; AAG53412.1; JOINED.
DR   EMBL; AF327228; AAG53412.1; JOINED.
DR   EMBL; AF327229; AAG53412.1; JOINED.
DR   EMBL; AF327230; AAG53412.1; JOINED.
DR   EMBL; AF327231; AAG53412.1; JOINED.
DR   EMBL; AF327232; AAG53412.1; JOINED.
DR   EMBL; AF327233; AAG53412.1; JOINED.
DR   EMBL; AF327234; AAG53412.1; JOINED.
DR   EMBL; AF327235; AAG53412.1; JOINED.
DR   EMBL; AF327236; AAG53412.1; JOINED.
DR   EMBL; AF327237; AAG53412.1; JOINED.
DR   EMBL; AF327238; AAG53412.1; JOINED.
DR   EMBL; AF327239; AAG53412.1; JOINED.
DR   EMBL; AF327240; AAG53412.1; JOINED.
DR   EMBL; AF327241; AAG53412.1; JOINED.
DR   EMBL; AF327242; AAG53412.1; JOINED.
DR   EMBL; AF327243; AAG53412.1; JOINED.
DR   EMBL; AF327244; AAG53412.1; JOINED.
DR   EMBL; AF327245; AAG53412.1; JOINED.
DR   EMBL; X65361; CAA46438.1; ALT_SEQ.
DR   EMBL; M91804; -; NOT_ANNOTATED_CDS.
DR   EMBL; M55662; AAB65854.2; -.
DR   HSSP; P04775; 1BYY.
DR   Genew; HGNC:10588; SCN2A2.
DR   MIM; 601219; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; TAS.
DR   GO; GO:0006814; P:sodium ion transport; TAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   REPEAT      111    456       I.
FT   REPEAT      741   1013       II.
FT   REPEAT     1190   1504       III.
FT   REPEAT     1513   1811       IV.
FT   TRANSMEM    125    148       S1 of repeat I.
FT   TRANSMEM    157    176       S2 of repeat I.
FT   TRANSMEM    190    208       S3 of repeat I.
FT   TRANSMEM    215    234       S4 of repeat I.
FT   TRANSMEM    251    274       S5 of repeat I.
FT   TRANSMEM    402    427       S6 of repeat I.
FT   TRANSMEM    754    778       S1 of repeat II.
FT   TRANSMEM    790    813       S2 of repeat II.
FT   TRANSMEM    822    841       S3 of repeat II.
FT   TRANSMEM    848    867       S4 of repeat II.
FT   TRANSMEM    884    904       S5 of repeat II.
FT   TRANSMEM    958    983       S6 of repeat II.
FT   TRANSMEM   1204   1227       S1 of repeat III.
FT   TRANSMEM   1241   1266       S2 of repeat III.
FT   TRANSMEM   1273   1294       S3 of repeat III.
FT   TRANSMEM   1299   1320       S4 of repeat III.
FT   TRANSMEM   1340   1367       S5 of repeat III.
FT   TRANSMEM   1447   1473       S6 of repeat III.
FT   TRANSMEM   1527   1550       S1 of repeat IV.
FT   TRANSMEM   1562   1585       S2 of repeat IV.
FT   TRANSMEM   1592   1615       S3 of repeat IV.
FT   TRANSMEM   1626   1647       S4 of repeat IV.
FT   TRANSMEM   1663   1685       S5 of repeat IV.
FT   TRANSMEM   1752   1776       S6 of repeat IV.
FT   DOMAIN     1905   1934       IQ.
FT   CARBOHYD    212    212       N-linked (GlcNAc. . .) (Potential).
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FT   CARBOHYD    285    285       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    291    291       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    297    297       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    303    303       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    340    340       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    604    604       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    624    624       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    883    883       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1055   1055       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1072   1072       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1136   1136       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1368   1368       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1382   1382       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1393   1393       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1778   1778       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    209    209       D -> N (in isoform 2).
FT                                /FTId=VSP_001032.
FT   CONFLICT    524    524       R -> L (in Ref. 1).

  Query Match             100.0%;  Score 28;  DB 1;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1449 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1476


RESULT 15
CIN2_RAT
ID   CIN2_RAT       STANDARD;      PRT;  2005 AA.
AC   P04775;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Sodium channel protein type II alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha
DE   subunit).
GN   Name=Scn2a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86146901; PubMed=3754035;
RA   Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M.,
RA   Takahashi H., Numa S.;
RT   "Existence of distinct sodium channel messenger RNAs in rat brain.";
RL   Nature 320:188-192(1986).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X03639; CAA27287.1; -.
DR   PDB; 1BYY; NMR; A=1474-1526.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   3D-structure; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   REPEAT      111    456       I.
FT   REPEAT      741   1013       II.
FT   REPEAT     1190   1504       III.
FT   REPEAT     1513   1811       IV.
FT   TRANSMEM    125    148       S1 of repeat I.
FT   TRANSMEM    157    176       S2 of repeat I.
FT   TRANSMEM    190    208       S3 of repeat I.
FT   TRANSMEM    215    234       S4 of repeat I.
FT   TRANSMEM    251    274       S5 of repeat I.
FT   TRANSMEM    402    427       S6 of repeat I.
FT   TRANSMEM    754    778       S1 of repeat II.
FT   TRANSMEM    790    813       S2 of repeat II.
FT   TRANSMEM    822    841       S3 of repeat II.
FT   TRANSMEM    848    867       S4 of repeat II.
FT   TRANSMEM    884    904       S5 of repeat II.
FT   TRANSMEM    958    983       S6 of repeat II.
FT   TRANSMEM   1204   1227       S1 of repeat III.
FT   TRANSMEM   1241   1266       S2 of repeat III.
FT   TRANSMEM   1273   1294       S3 of repeat III.
FT   TRANSMEM   1299   1320       S4 of repeat III.
FT   TRANSMEM   1340   1367       S5 of repeat III.
FT   TRANSMEM   1447   1473       S6 of repeat III.
FT   TRANSMEM   1527   1550       S1 of repeat IV.
FT   TRANSMEM   1562   1585       S2 of repeat IV.
FT   TRANSMEM   1592   1615       S3 of repeat IV.
FT   TRANSMEM   1626   1647       S4 of repeat IV.
FT   TRANSMEM   1663   1685       S5 of repeat IV.
FT   TRANSMEM   1752   1776       S6 of repeat IV.
FT   DOMAIN     1905   1934       IQ.
FT   CARBOHYD    212    212       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    285    285       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    291    291       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    297    297       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    303    303       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    340    340       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    604    604       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    624    624       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    883    883       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1055   1055       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1072   1072       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1136   1136       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1368   1368       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1382   1382       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1393   1393       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   2005 AA;  227872 MW;  861BE583D79F8324 CRC64;

  Query Match             100.0%;  Score 28;  DB 1;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1449 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1476
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RESULT 16
Q9YGN7
ID   Q9YGN7      PRELIMINARY;      PRT;  2007 AA.
AC   Q9YGN7;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-dependent sodium channel.
OS   Cynops pyrrhogaster (Japanese common newt).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX   NCBI_TaxID=8330;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RA   Hirota K., Kaneko Y., Matsumoto G., Hanyu Y.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AF123593; AAD17315.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   2007 AA;  228398 MW;  013E9B9EC9C294C9 CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 2007;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1450 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1477


RESULT 17
CIN1_HUMAN
ID   CIN1_HUMAN     STANDARD;      PRT;  2009 AA.
AC   P35498; Q16172; Q96LA3; Q9C008;
DT   01-JUN-1994 (Rel. 29, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type I alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.1) (Sodium channel protein, brain I alpha
DE   subunit).
GN   Name=SCN1A; Synonyms=SCN1, NAC1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS GEFS+2 MET-875 AND
RP   HIS-1648.
RX   MEDLINE=20206553; PubMed=10742094;
RA   Escayg A., MacDonald B.T., Meisler M.H., Baulac S., Huberfeld G.,
RA   An-Gourfinkel I., Brice A., LeGuern E., Moulard B., Chaigne D.,
RA   Buresi C., Malafosse A.;
RT   "Mutations of SCN1A, encoding a neuronal sodium channel, in two
RT   families with GEFS+2.";
RL   Nat. Genet. 24:343-345(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RA   Jeong S.-Y., Goto J., Kanazawa I.;
RT   "Cloning of cDNA for human voltage-gated sodium channel alpha subunit,
RT   SCN1A.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Brain;
RA   Sugawara T., Mazaki E.M., Yamakawa K.;
RT   "Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1)
RT   mRNA.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT THR-1067.
RA   Ouchida M., Ohmori I.;
RT   "Isoforms of human sodium channel SCN1A gene.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 1335-1428 FROM N.A.
RX   MEDLINE=94340991; PubMed=8062593;
RA   Malo M.S., Blanchard B.J., Andresen J.M., Srivastava K., Chen X.N.,
RA   Li X., Jabs E.W., Korenberg J.R., Ingram V.M.;
RT   "Localization of a putative human brain sodium channel gene (SCN1A) to
RT   chromosome band 2q24.";
RL   Cytogenet. Cell Genet. 67:178-186(1994).
RN   [6]
RP   SEQUENCE OF 1518-1940 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92275082; PubMed=1317301;
RA   Lu C.-M., Han J., Rado T.A., Brown G.B.;
RT   "Differential expression of two sodium channel subtypes in human
RT   brain.";
RL   FEBS Lett. 303:53-58(1992).
RN   [7]
RP   VARIANTS GEFS+2 VAL-188; LEU-1353 AND MET-1656.
RX   MEDLINE=21152274; PubMed=11254444;
RA   Wallace R.H., Scheffer I.E., Barnett S., Richards M., Dibbens L.,
RA   Desai R.R., Lerman-Sagie T., Lev D., Mazarib A., Brand N.,
RA   Ben-Zeev B., Goikhman I., Singh R., Kremmidiotis G., Gardner A.,
RA   Sutherland G.R., George A.L. Jr., Mulley J.C., Berkovic S.F.;
RT   "Neuronal sodium-channel alpha1-subunit mutations in generalized
RT   epilepsy with febrile seizures plus.";
RL   Am. J. Hum. Genet. 68:859-865(2001).
RN   [8]
RP   VARIANT GEFS+2 ARG-1204.
RX   MEDLINE=21152275; PubMed=11254445;
RA   Escayg A., Heils A., MacDonald B.T., Haug K., Sander T., Meisler M.H.;
RT   "A novel SCN1A mutation associated with generalized epilepsy with
RT   febrile seizures plus -- and prevalence of variants in patients with
RT   epilepsy.";
RL   Am. J. Hum. Genet. 68:866-873(2001).
RN   [9]
RP   VARIANT SMEI PHE-986.
RX   MEDLINE=21257503; PubMed=11359211;
RA   Claes L., Del-Favero J., Ceulemans B., Lagae L., Van Broeckhoven C.,
RA   De Jonghe P.;
RT   "De novo mutations in the sodium-channel gene SCN1A cause severe
RT   myoclonic epilepsy of infancy.";
RL   Am. J. Hum. Genet. 68:1327-1332(2001).
RN   [10]
RP   VARIANT GEFS+2 THR-1270.
RX   MEDLINE=21630138; PubMed=11756608;
RA   Abou-Khalil B., Ge Q., Desai R., Ryther R., Bazyk A., Bailey R.,
RA   Haines J.L., Sutcliffe J.S., George A.L. Jr.;
RT   "Partial and generalized epilepsy with febrile seizures plus and a
RT   novel SCN1A mutation.";
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RL   Neurology 57:2265-2272(2001).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=P35498-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P35498-2; Sequence=VSP_001031;
CC         Note=No experimental confirmation available;
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- DISEASE: Defects in SCN1A are the cause of generalized epilepsy
CC       with febrile seizures plus type 2 (GEFS+2) [MIM:604233]. This
CC       autosomal dominant disorder is characterized by febrile seizures
CC       in children and afebrile seizures in adults. Penetrance is
CC       incomplete and a large intrafamilial variability of the phenotype
CC       is observed.
CC   -!- DISEASE: Defects in SCN1A are a cause of severe myoclonic epilepsy
CC       in infancy (SMEI) [MIM:607208], a severe form of generalized
CC       epilepsy with febrile seizures. SMEI is a rare disorder
CC       characterized by normal development before onset, seizures
CC       beginning in the first year of life in the form of generalized or
CC       unilateral febrile clonic seizures, secondary appearance of
CC       myoclonic seizures, and occasionally partial seizures. It is
CC       associated with ataxia, slowed psychomotor development, and mental
CC       decline.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF225985; AAK00217.1; -.
DR   EMBL; AY043484; AAK95360.1; -.
DR   EMBL; AB093548; BAC21101.1; -.
DR   EMBL; AB093549; BAC21102.1; -.
DR   EMBL; S71446; AAB31605.1; -.
DR   EMBL; X65362; CAA46439.1; -.
DR   EMBL; M91803; -; NOT_ANNOTATED_CDS.
DR   PIR; I52964; I52964.
DR   PIR; S29184; S29184.
DR   HSSP; P04775; 1BYY.
DR   Genew; HGNC:10585; SCN1A.
DR   MIM; 182389; -.
DR   MIM; 604233; -.
DR   MIM; 607208; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; NAS.
DR   GO; GO:0006814; P:sodium ion transport; NAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008051; Na_channel1.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01664; NACHANNEL1.
DR   PROSITE; PS50096; IQ; FALSE_NEG.
KW   Alternative splicing; Disease mutation; Epilepsy; Glycoprotein;
KW   Ion transport; Ionic channel; Multigene family; Polymorphism; Repeat;
KW   Sodium channel; Transmembrane; Voltage-gated channel.
FT   REPEAT      110    454       I.
FT   REPEAT      750   1022       II.
FT   REPEAT     1200   1514       III.
FT   REPEAT     1523   1821       IV.
FT   TRANSMEM    124    147       S1 of repeat I (By similarity).
FT   TRANSMEM    156    175       S2 of repeat I (By similarity).
FT   TRANSMEM    189    207       S3 of repeat I (By similarity).
FT   TRANSMEM    214    233       S4 of repeat I (By similarity).
FT   TRANSMEM    250    273       S5 of repeat I (By similarity).
FT   TRANSMEM    400    425       S6 of repeat I (By similarity).
FT   TRANSMEM    763    787       S1 of repeat II (By similarity).
FT   TRANSMEM    799    822       S2 of repeat II (By similarity).
FT   TRANSMEM    831    850       S3 of repeat II (By similarity).
FT   TRANSMEM    857    876       S4 of repeat II (By similarity).
FT   TRANSMEM    893    913       S5 of repeat II (By similarity).
FT   TRANSMEM    967    992       S6 of repeat II (By similarity).
FT   TRANSMEM   1214   1237       S1 of repeat III (By similarity).
FT   TRANSMEM   1251   1276       S2 of repeat III (By similarity).
FT   TRANSMEM   1283   1304       S3 of repeat III (By similarity).
FT   TRANSMEM   1309   1330       S4 of repeat III (By similarity).
FT   TRANSMEM   1350   1377       S5 of repeat III (By similarity).
FT   TRANSMEM   1457   1483       S6 of repeat III (By similarity).
FT   TRANSMEM   1537   1560       S1 of repeat IV (By similarity).
FT   TRANSMEM   1572   1595       S2 of repeat IV (By similarity).
FT   TRANSMEM   1602   1625       S3 of repeat IV (By similarity).
FT   TRANSMEM   1636   1657       S4 of repeat IV (By similarity).
FT   TRANSMEM   1673   1695       S5 of repeat IV (By similarity).
FT   TRANSMEM   1762   1786       S6 of repeat IV (By similarity).
FT   CARBOHYD    211    211       N-linked (GlcNAc. . .) (Potential).

  Query Match             100.0%;  Score 28;  DB 1;  Length 2009;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1459 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1486


RESULT 18
CIN1_RAT
ID   CIN1_RAT       STANDARD;      PRT;  2009 AA.
AC   P04774;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type I alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.1) (Sodium channel protein, brain I alpha
DE   subunit).
GN   Name=Scn1a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86146901; PubMed=3754035;
RA   Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M.,
RA   Takahashi H., Numa S.;
RT   "Existence of distinct sodium channel messenger RNAs in rat brain.";
RL   Nature 320:188-192(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87311395; PubMed=2442385;
RA   Noda M., Numa S.;
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```
RT   "Structure and function of sodium channel.";
RL   J. Recept. Res. 7:467-497(1987).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X03638; CAA27286.1; -.
DR   EMBL; M22253; AAA79965.1; -.
DR   PIR; A25019; A25019.
DR   HSSP; P04775; 1BYY.
DR   RGD; 69364; Scn1a.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008051; Na_channel1.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01664; NACHANNEL1.
DR   PROSITE; PS50096; IQ; FALSE_NEG.
KW   Glycoprotein; Ion transport; Ionic channel; Multigene family; Repeat;
KW   Sodium channel; Transmembrane; Voltage-gated channel.
FT   REPEAT      110    454       I.
FT   REPEAT      750   1022       II.
FT   REPEAT     1200   1514       III.
FT   REPEAT     1523   1821       IV.
FT   TRANSMEM    124    147       S1 of repeat I.
FT   TRANSMEM    156    175       S2 of repeat I.
FT   TRANSMEM    189    207       S3 of repeat I.
FT   TRANSMEM    214    233       S4 of repeat I.
FT   TRANSMEM    250    273       S5 of repeat I.
FT   TRANSMEM    400    425       S6 of repeat I.
FT   TRANSMEM    763    787       S1 of repeat II.
FT   TRANSMEM    799    822       S2 of repeat II.
FT   TRANSMEM    831    850       S3 of repeat II.
FT   TRANSMEM    857    876       S4 of repeat II.
FT   TRANSMEM    893    913       S5 of repeat II.
FT   TRANSMEM    967    992       S6 of repeat II.
FT   TRANSMEM   1214   1237       S1 of repeat III.
FT   TRANSMEM   1251   1276       S2 of repeat III.
FT   TRANSMEM   1283   1304       S3 of repeat III.
FT   TRANSMEM   1309   1330       S4 of repeat III.
FT   TRANSMEM   1350   1377       S5 of repeat III.
FT   TRANSMEM   1457   1483       S6 of repeat III.
FT   TRANSMEM   1537   1560       S1 of repeat IV.
FT   TRANSMEM   1572   1595       S2 of repeat IV.
FT   TRANSMEM   1602   1625       S3 of repeat IV.
FT   TRANSMEM   1636   1657       S4 of repeat IV.
FT   TRANSMEM   1673   1695       S5 of repeat IV.
FT   TRANSMEM   1762   1786       S6 of repeat IV.
FT   CARBOHYD    211    211       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    284    284       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    295    295       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    301    301       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    306    306       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    338    338       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    601    601       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    621    621       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    681    681       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    892    892       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1060   1060       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1064   1064       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1080   1080       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1146   1146       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1378   1378       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1392   1392       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1403   1403       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   2009 AA;  228769 MW;  6808466F6368373B CRC64;

  Query Match             100.0%;  Score 28;  DB 1;  Length 2009;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28
              ||||||||||||||||||||||||||||
Db       1459 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 1486


RESULT 19
Q90Z30
ID   Q90Z30      PRELIMINARY;      PRT;   718 AA.
AC   Q90Z30;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel 1 (Fragment).
OS   Sternopygus macrurus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC   Sternopygidae; Sternopygus.
OX   NCBI_TaxID=77841;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21310016; PubMed=11416226;
RA   Lopreato G.F., Lu Y., Southwell A., Atkinson N.S., Hillis D.M.,
RA   Wilcox T.P., Zakon H.H.;
RT   "Evolution and divergence of sodium channel genes in vertebrates.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7588-7592(2001).
DR   EMBL; AF378139; AAK55437.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 2.
DR   Pfam; PF06512; Na_trans_assoc; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1      1
FT   NON_TER     718    718
SQ   SEQUENCE   718 AA;  81545 MW;  67C779B99DA3BBCE CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 718;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-16;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db        644 YFVIFIIFGSFFTLNLFIGVIIDNF 668
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RESULT 20
Q90Z26
ID   Q90Z26      PRELIMINARY;      PRT;   743 AA.
AC   Q90Z26;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel 5 (Fragment).
OS   Sternopygus macrurus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC   Sternopygidae; Sternopygus.
OX   NCBI_TaxID=77841;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21310016; PubMed=11416226;
RA   Lopreato G.F., Lu Y., Southwell A., Atkinson N.S., Hillis D.M.,
RA   Wilcox T.P., Zakon H.H.;
RT   "Evolution and divergence of sodium channel genes in vertebrates.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7588-7592(2001).
DR   EMBL; AF378143; AAK55441.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 2.
DR   Pfam; PF06512; Na_trans_assoc; 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1      1
FT   NON_TER     743    743
SQ   SEQUENCE   743 AA;  84781 MW;  F2429665544CAB0C CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 743;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-16;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db        669 YFVIFIIFGSFFTLNLFIGVIIDNF 693


RESULT 21
Q9IBF1
ID   Q9IBF1      PRELIMINARY;      PRT;  1880 AA.
AC   Q9IBF1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel.
OS   Takifugu pardalis (Panther puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=98921;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=20090650; PubMed=10623632;
RA   Yotsu-Yamashita M., Nishimori K., Nitanai Y., Isemura M., Sugimoto A.,
RA   Yasumoto T.;
RT   "Binding properties of 3H-PbTx-3 and 3H-saxitoxin to brain membranes
RT   and to skeletal muscle membranes of puffer fish Fugu pardalis, and the
RT   primary structure of a voltage-gated Na+ channel alpha-subunit (fMNa1)
RT   from skeletal muscle of F. pardalis.";
RL   Biochem. Biophys. Res. Commun. 267:403-412(2000).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AB030482; BAA90398.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1880 AA;  212084 MW;  406483C6C3D43E02 CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 1880;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-16;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1302 YFVIFIIFGSFFTLNLFIGVIIDNF 1326


RESULT 22
Q9DF53
ID   Q9DF53      PRELIMINARY;      PRT;  1949 AA.
AC   Q9DF53;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel protein Scn8a.
GN   Name=scn8a;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=oregon;
RA   Tsai C.-W., Tseng J.-J., Horng J.-F., Wu J.-L., Tsay H.-J.;
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AF297658; AAG18440.1; -.
DR   HSSP; P04775; 1BYY.
DR   ZFIN; ZDB-GENE-000828-1; scn8a.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008054; Na_channel8.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
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DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01667; NACHANNEL8.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1949 AA;  221760 MW;  6BCA69664BDC7BC3 CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 1949;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-16;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1412 YFVIFIIFGSFFTLNLFIGVIIDNF 1436


RESULT 23
Q75RX9
ID   Q75RX9      PRELIMINARY;      PRT;  1962 AA.
AC   Q75RX9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   TTX-resistant sodium channel splicing variant.
GN   Name=Nav1.5;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ou S., Kameyama A., Kameyama M.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Ou S., Kameyama A., Kameyama M.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AB158470; BAD12085.1; -.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR010983; EF_Hand_like.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008053; Na_channel5.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01666; NACHANNEL5.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1962 AA;  221146 MW;  3EA3B3D897199C9A CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 1962;
  Best Local Similarity   100.0%;  Pred. No. 5e-16;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1395 YFVIFIIFGSFFTLNLFIGVIIDNF 1419


RESULT 24
BAD12085
ID   BAD12085    PRELIMINARY;      PRT;  1962 AA.
AC   BAD12085;
DT   03-MAR-2004 (TrEMBLrel. 27, Created)
DT   03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   03-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   TTX-resistant sodium channel splicing variant.
GN   NAV1.5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ou S., Kameyama A., Kameyama M.;
RT   "Cloning of TTX-resistant Na+ channels in NB-1 cell lines.";
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Ou S., Kameyama A., Kameyama M.;
RT   "Splicing Variant of TTX-resistant Na+ channel in NB-1 cell lines.";
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB158470; BAD12085.1; -.
KW   Ionic channel.
SQ   SEQUENCE   1962 AA;  221146 MW;  3EA3B3D897199C9A CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 1962;
  Best Local Similarity   100.0%;  Pred. No. 5e-16;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1395 YFVIFIIFGSFFTLNLFIGVIIDNF 1419


RESULT 25
Q63541
ID   Q63541      PRELIMINARY;      PRT;  1976 AA.
AC   Q63541;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel protein 6.
GN   Name=SCP6;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=95271284; PubMed=7751906;
RA   Schaller K.L., Krzemien D.M., Yarowsky P.J., Krueger B.K.,
RA   Caldwell J.H.;
RT   "A novel, abundant sodium channel expressed in neurons and glia.";
RL   J. Neurosci. 15:3231-3242(1995).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; L39018; AAC42059.1; -.
DR   PIR; I56555; I56555.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR000183; Decarbxylse2.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008054; Na_channel8.
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DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01667; NACHANNEL8.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
DR   PROSITE; PS00878; ODR_DC_2_1; UNKNOWN_1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1976 AA;  225227 MW;  B6949327A47FA88A CRC64;

  Query Match             89.3%;  Score 25;  DB 2;  Length 1976;
  Best Local Similarity   100.0%;  Pred. No. 5e-16;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1439 YFVIFIIFGSFFTLNLFIGVIIDNF 1463


Search completed: January 27, 2005, 17:51:33
Job time : 93.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:36:50 ; Search time 22.5 Seconds
(without alignments)
82.529 Million cell updates/sec

Title: US-10-608-584-19
Perfect score: 28
Sequence: 1 MYLYFVIFIIFGSFFTLNLFIGVIIDNF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	28	100.0	2005	4	US-09-457-571-7	Sequence 7, Appli
4	25	89.3	813	3	US-08-836-325-8	Sequence 8, Appli
5	25	89.3	813	4	US-09-457-571-8	Sequence 8, Appli
6	25	89.3	1011	3	US-08-836-325-2	Sequence 2, Appli
7	25	89.3	1011	4	US-09-457-571-2	Sequence 2, Appli
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19	25	89.3	2016	4	US-09-514-907A-2	Sequence 2, Appli
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ALIGNMENTS

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RESULT 1
US-10-162-012-24
; Sequence 24, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  Gu, Wei
;  TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
;  FILE REFERENCE: 10448-190001
;  CURRENT APPLICATION NUMBER: US/10/162,012
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: US 60/209,845
;  PRIOR FILING DATE: 2000-06-06
;  PRIOR APPLICATION NUMBER: US 09/875,321
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: PCT/US01/18340
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/209,257
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,423
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18398
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/209,238
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,363
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18247
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/227,068
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: US 09/928,530
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: PCT/US01/25475
;  PRIOR FILING DATE: 2001-08-15
;  PRIOR APPLICATION NUMBER: US 60/226,770
;  PRIOR FILING DATE: 2000-08-21
;  PRIOR APPLICATION NUMBER: US 09/934,421
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;  PRIOR APPLICATION NUMBER: PCT/US01/26096
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: US 60/279,281
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 10/109,029
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: PCT/US02/09728
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 60/290,288
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US (not assigned)
;  PRIOR FILING DATE: 2002-05-13
;  NUMBER OF SEQ ID NOS: 48
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; SEQ ID NO 24
;   LENGTH: 1836
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-162-012-24

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US-08-836-325-7
; Sequence 7, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2005 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-836-325-7

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  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; Sequence 7, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
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;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995 .
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2005 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-457-571-7

  Query Match             100.0%;  Score 28;  DB 4;  Length 2005;
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; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  813 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-836-325-8

  Query Match             89.3%;  Score 25;  DB 3;  Length 813;
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RESULT 5
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; Sequence 8, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/457,571
;       FILING DATE:  09-DEC-1999
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/836,325
;       FILING DATE:  02-MAY-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/14251
;       FILING DATE:  02-NOV-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/482,401
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/334,029
;       FILING DATE:  02-NOV-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ludwig, Steven R.
;       REGISTRATION NUMBER:  36,203
;       REFERENCE/DOCKET NUMBER:  0917.0240003
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  813 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-09-457-571-8

  Query Match             89.3%;  Score 25;  DB 4;  Length 813;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-18;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
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Db        347 YFVIFIIFGSFFTLNLFIGVIIDNF 371


RESULT 6
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; Sequence 2, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1011 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-836-325-2

  Query Match             89.3%;  Score 25;  DB 3;  Length 1011;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db        481 YFVIFIIFGSFFTLNLFIGVIIDNF 505


RESULT 7
US-09-457-571-2
; Sequence 2, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1011 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-457-571-2

  Query Match             89.3%;  Score 25;  DB 4;  Length 1011;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db        481 YFVIFIIFGSFFTLNLFIGVIIDNF 505


RESULT 8
US-09-024-020B-9
; Sequence 9, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1976 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-024-020B-9

  Query Match             89.3%;  Score 25;  DB 3;  Length 1976;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1439 YFVIFIIFGSFFTLNLFIGVIIDNF 1463


RESULT 9
US-09-425-043-9
; Sequence 9, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1976 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-425-043-9

  Query Match             89.3%;  Score 25;  DB 3;  Length 1976;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1439 YFVIFIIFGSFFTLNLFIGVIIDNF 1463


RESULT 10
US-09-024-020B-3
; Sequence 3, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
```

```
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1978 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-024-020B-3

  Query Match             89.3%;  Score 25;  DB 3;  Length 1978;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1441 YFVIFIIFGSFFTLNLFIGVIIDNF 1465


RESULT 11
US-09-425-043-3
; Sequence 3, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1978 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-425-043-3

  Query Match             89.3%;  Score 25;  DB 3;  Length 1978;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1441 YFVIFIIFGSFFTLNLFIGVIIDNF 1465


RESULT 12
US-08-836-325-10
; Sequence 10, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1984 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-836-325-10

  Query Match             89.3%;  Score 25;  DB 3;  Length 1984;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1434 YFVIFIIFGSFFTLNLFIGVIIDNF 1458


RESULT 13
US-09-457-571-10
; Sequence 10, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1984 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-457-571-10

  Query Match             89.3%;  Score 25;  DB 4;  Length 1984;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1434 YFVIFIIFGSFFTLNLFIGVIIDNF 1458


RESULT 14
US-09-024-020B-4
; Sequence 4, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1988 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-024-020B-4

  Query Match             89.3%;  Score 25;  DB 3;  Length 1988;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
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Db       1451 YFVIFIIFGSFFTLNLFIGVIIDNF 1475


RESULT 15
US-09-425-043-4
; Sequence 4, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1988 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-425-043-4

  Query Match             89.3%;  Score 25;  DB 3;  Length 1988;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1451 YFVIFIIFGSFFTLNLFIGVIIDNF 1475


RESULT 16
US-08-836-325-12
; Sequence 12, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1989 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-836-325-12

  Query Match             89.3%;  Score 25;  DB 3;  Length 1989;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1436 YFVIFIIFGSFFTLNLFIGVIIDNF 1460


RESULT 17
US-09-457-571-12
; Sequence 12, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1989 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-09-457-571-12

  Query Match             89.3%;  Score 25;  DB 4;  Length 1989;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1436 YFVIFIIFGSFFTLNLFIGVIIDNF 1460


RESULT 18
US-09-634-920-4
; Sequence 4, Application US/09634920
; Patent No. 6342357
; GENERAL INFORMATION:
;  APPLICANT:  Splawski, Igor
;  APPLICANT:  Keating, Mark T.
;  TITLE OF INVENTION:  ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
;  TITLE OF INVENTION:  SCN5A AND METHODS FOR DETECTING SAME
;  FILE REFERENCE:  2323-155
;  CURRENT APPLICATION NUMBER: US/09/634,920
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/190,057
;  PRIOR FILING DATE:  2000-03-17
;  PRIOR APPLICATION NUMBER:  60/147,488
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 2016
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-634-920-4

  Query Match             89.3%;  Score 25;  DB 3;  Length 2016;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1449 YFVIFIIFGSFFTLNLFIGVIIDNF 1473


RESULT 19
US-09-514-907A-2
; Sequence 2, Application US/09514907A
; Patent No. 6567705
;  GENERAL INFORMATION:
;       APPLICANT: Kenneth B. Stokes
;                  Jos,e Morissette
;       TITLE OF INVENTION: SYSTEMS FOR ENHANCING CARDIAC SIGNAL
;                           SENSING BY CARDIAC PACEMAKERS THROUGH
;                           GENETIC TREATMENT
;       NUMBER OF SEQUENCES: 12
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6567705ris LLP
;            STREET: One Liberty Place - 46th Floor
;            CITY: Philadelphia
;            STATE: PA
;            COUNTRY: U.S.A.
;            ZIP: 19103
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WordPerfect 6.1
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/514,907A
;            FILING DATE: 08-Feb-2000
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Paul K. Legaard
;            REGISTRATION NUMBER: 38,534
;            REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (215) 568-3100
;            TELEFAX: (215) 568-3439
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2016 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: unknown
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-514-907A-2

  Query Match             89.3%;  Score 25;  DB 4;  Length 2016;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1449 YFVIFIIFGSFFTLNLFIGVIIDNF 1473


RESULT 20
US-09-896-994-2
; Sequence 2, Application US/09896994
; Patent No. 6665563
;  GENERAL INFORMATION:
;       APPLICANT: Ken Stokes
;                  Jos e Morissette
;       TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC
;                           SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATME
;       NUMBER OF SEQUENCES: 12
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6665563ris
;            STREET: One Liberty Place - 46th Floor
;            CITY: Philadelphia
;            STATE: PA
```

```
;              COUNTRY: U.S.A.
;              ZIP: 19103
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: WordPerfect 6.1
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/896,994
;              FILING DATE: 02-Jul-2001
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 09/514,907
;              FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Paul K. Legaard
;              REGISTRATION NUMBER: 38,534
;              REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (215) 568-3100
;              TELEFAX: (215) 568-3439
;    INFORMATION FOR SEQ ID NO: 2:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 2016 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: unknown
;         SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-896-994-2

  Query Match             89.3%;  Score 25;  DB 4;  Length 2016;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1449 YFVIFIIFGSFFTLNLFIGVIIDNF 1473


RESULT 21
US-09-840-125-4
; Sequence 4, Application US/09840125
; Patent No. 6787309
; GENERAL INFORMATION:
;  APPLICANT: Splawski, Igor
;  APPLICANT:  Keating, Mark T.
;  TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
;  TITLE OF INVENTION:  SCN5A AND METHODS FOR DETECTING SAME
;  FILE REFERENCE: 2323-155
;  CURRENT APPLICATION NUMBER: US/09/840,125
;  CURRENT FILING DATE:  2001-04-24
;  PRIOR APPLICATION NUMBER: 09/634,920
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,488
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 2016
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-840-125-4

  Query Match             89.3%;  Score 25;  DB 4;  Length 2016;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 YFVIFIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||||||
Db       1449 YFVIFIIFGSFFTLNLFIGVIIDNF 1473


RESULT 22
US-08-808-793-25
; Sequence 25, Application US/08808793
; Patent No. 5858713
;  GENERAL INFORMATION:
;    APPLICANT:  Soderlund, David M.
;    APPLICANT:  Ingles, Patricia J.
;    TITLE OF INVENTION:  CALCIUM PERMEABLE INSECT SODIUM CHANNELS
;    TITLE OF INVENTION:  AND USE THEREOF
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle LLP
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/808,793
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/034,361
;      FILING DATE:  24-DEC-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/012,649
;      FILING DATE:  01-MAR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Braman, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/1062 (D-1906A)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  716-263-1636
;      TELEFAX:  716-263-1600
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  413 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-808-793-25

  Query Match             75.0%;  Score 21;  DB 2;  Length 413;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-14;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 FIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||
Db         94 FIIFGSFFTLNLFIGVIIDNF 114


RESULT 23
US-07-998-289B-6
; Sequence 6, Application US/07998289B
; Patent No. 6027876
;  GENERAL INFORMATION:
;    APPLICANT:  Black, Bruce C
;    APPLICANT:  Taylor, Martin
;    APPLICANT:  Heckel, David G
;    TITLE OF INVENTION:  Method for Monitoring Pesticide
;    TITLE OF INVENTION:  Resistance
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby PC
;      STREET:  805 Third Avenue
;      CITY:  New York
```

```
;      STATE:  New York
;      COUNTRY:  US
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/998,289B
;      FILING DATE:  30-DEC-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Robinson, Joseph R
;      REGISTRATION NUMBER:  33,448
;      REFERENCE/DOCKET NUMBER:  0646/0A939
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-527-7700
;      TELEFAX:  212-753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-998-289B-6

  Query Match             75.0%;  Score 21;  DB 3;  Length 452;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-14;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 FIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||
Db        126 FIIFGSFFTLNLFIGVIIDNF 146


RESULT 24
US-09-354-147C-7
; Sequence 7, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
;  APPLICANT: Dib-Hajj, Sulayman
;  APPLICANT:  Waxman, Stephen G.
;  TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
;  FILE REFERENCE: 44574-5004-01-US
;  CURRENT APPLICATION NUMBER: US/09/354,147C
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER: US 60/072,990
;  PRIOR FILING DATE: 1998-01-29
;  PRIOR APPLICATION NUMBER: US 60/109,402
;  PRIOR FILING DATE: 1998-11-20
;  PRIOR APPLICATION NUMBER: PCT/US99/02008
;  PRIOR FILING DATE: 1999-01-29
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 1233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: (308)
;   OTHER INFORMATION: Xaa is Leu. Xaa results from a "y" in SEQ ID NO: 6.
US-09-354-147C-7

  Query Match             75.0%;  Score 21;  DB 4;  Length 1233;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 FIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||
Db       1092 FIIFGSFFTLNLFIGVIIDNF 1112


RESULT 25
US-09-354-147C-8
; Sequence 8, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
;  APPLICANT: Dib-Hajj, Sulayman
;  APPLICANT:  Waxman, Stephen G.
;  TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
;  FILE REFERENCE: 44574-5004-01-US
;  CURRENT APPLICATION NUMBER: US/09/354,147C
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER: US 60/072,990
;  PRIOR FILING DATE: 1998-01-29
;  PRIOR APPLICATION NUMBER: US 60/109,402
;  PRIOR FILING DATE: 1998-11-20
;  PRIOR APPLICATION NUMBER: PCT/US99/02008
;  PRIOR FILING DATE: 1999-01-29
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 1243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: partial human NaN amino acid seq.
US-09-354-147C-8

  Query Match             75.0%;  Score 21;  DB 4;  Length 1243;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 FIIFGSFFTLNLFIGVIIDNF 28
              |||||||||||||||||||||
Db       1092 FIIFGSFFTLNLFIGVIIDNF 1112


Search completed: January 27, 2005, 17:54:19
Job time : 23.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:32:04 ; Search time 86.5 Seconds
(without alignments)
116.120 Million cell updates/sec

Title: US-10-608-584-29
Perfect score: 28
Sequence: 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	100.0	405	4	AAM15136	Aam15136 Peptide #
2	28	100.0	405	4	ABB34128	Abb34128 Peptide #
3	28	100.0	405	4	AAM27591	Aam27591 Peptide #
4	28	100.0	405	4	ABB28960	Abb28960 Peptide #
5	28	100.0	405	4	ABB19569	Abb19569 Protein #
6	28	100.0	405	4	AAM67299	Aam67299 Human bon
7	28	100.0	405	4	AAM54918	Aam54918 Human bra
8	28	100.0	405	4	AAM56160	Aam56160 Human bra
9	28	100.0	405	4	ABG48961	Abg48961 Human liv
10	28	100.0	405	4	AAM02877	Aam02877 Peptide #
11	28	100.0	405	4	AAM04075	Aam04075 Peptide #
12	28	100.0	405	5	ABG36946	Abg36946 Human pep
13	28	100.0	1855	7	ADB78597	Adb78597 Human sod
14	28	100.0	1950	7	ADB78607	Adb78607 Human sod
15	28	100.0	1951	7	ADE59628	Ade59628 Rat Prote
16	28	100.0	1951	8	ADL06576	Adl06576 Human tum
17	28	100.0	1962	5	AAE20511	Aae20511 Human ion
18	28	100.0	1973	5	AAE20516	Aae20516 Human ion
19	28	100.0	1981	7	ABR83185	Abr83185 Human SCN
20	28	100.0	1998	5	AAE20510	Aae20510 Human ion
21	28	100.0	1998	7	ABR83184	Abr83184 Human SCN
22	28	100.0	1999	5	ABB06026	Abb06026 Human sod
23	28	100.0	2000	5	ABB06027	Abb06027 Human sod
24	28	100.0	2000	8	ADK81762	Adk81762 Human Nav
25	28	100.0	2005	4	AAB99676	Aab99676 Human adu
26	28	100.0	2005	4	AAB99677	Aab99677 Human neo
27	28	100.0	2009	4	AAB99674	Aab99674 Human adu
28	28	100.0	2009	5	AAE20515	Aae20515 Human ion
29	28	100.0	2009	5	ABG69292	Abg69292 Human sod
30	28	100.0	2009	5	ABG69291	Abg69291 Human sod
31	28	100.0	2009	5	ABG69293	Abg69293 Human sod
32	28	100.0	2009	5	ABG69289	Abg69289 Human sod
33	28	100.0	2009	5	ABG69290	Abg69290 Human sod
34	28	100.0	2009	5	ABB83626	Abb83626 Human GEF
35	28	100.0	2009	5	AAE16776	Aae16776 Human tra
36	28	100.0	2009	7	ADB78599	Adb78599 Human sod
37	28	100.0	2009	7	ADB78595	Adb78595 Human sod
38	28	100.0	2009	7	ADB78593	Adb78593 Human sod
39	28	100.0	2009	7	ADB78594	Adb78594 Human sod
40	28	100.0	2009	7	ADB78598	Adb78598 Human sod
41	28	100.0	2009	7	ABR83180	Abr83180 Human SCN
42	28	100.0	2009	7	ADE57563	Ade57563 Human Pro
43	28	100.0	2009	7	ADE57561	Ade57561 Rat Prote
44	27	96.4	309	3	AAB03656	Aab03656 Clone 5 v
45	27	96.4	309	3	AAB03655	Aab03655 Clone 3 v
46	27	96.4	1795	7	ADB78596	Adb78596 Human sod
47	24	85.7	1011	2	AAR99638	Aar99638 Periphera
48	24	85.7	1835	2	AAR92316	Aar92316 Periphera
49	24	85.7	1977	2	AAR99641	Aar99641 Periphera
50	24	85.7	1977	8	ADE77202	Ade77202 Human pro
51	24	85.7	1977	8	ADL13028	Adl13028 Human ste
52	24	85.7	1978	7	ADE54553	Ade54553 Human Pro
53	24	85.7	1978	7	ADE54549	Ade54549 Human Pro
54	24	85.7	1984	2	AAR99639	Aar99639 Periphera
55	24	85.7	1984	7	ADE54547	Ade54547 Rat Prote
56	24	85.7	1984	7	ADE54551	Ade54551 Rat Prote
57	24	85.7	1984	7	ADE63027	Ade63027 Rat Prote
58	24	85.7	1989	2	AAR92317	Aar92317 Periphera
59	24	85.7	1989	2	AAR99640	Aar99640 Periphera
60	21	75.0	158	4	AAM24350	Aam24350 Murine ES
61	18	64.3	1951	4	AAB99678	Aab99678 Human adu
62	18	64.3	1951	4	AAB99679	Aab99679 Human neo
63	16	57.1	2005	5	ABB83627	Abb83627 Human GEF
64	16	57.1	2005	7	ADB78604	Adb78604 Human sod
65	16	57.1	2005	7	ADB78603	Adb78603 Human sod
66	16	57.1	2005	7	ADB78605	Adb78605 Human sod
67	16	57.1	2005	7	ADC46947	Adc46947 Human SCN
68	14	50.0	232	2	AAW69363	Aaw69363 Probe CNa
69	14	50.0	309	3	AAB03657	Aab03657 Clone 6 v
70	14	50.0	1976	7	ADE57386	Ade57386 Rat Prote
71	14	50.0	1978	2	AAW69361	Aaw69361 Tetrodoto
72	14	50.0	1980	3	AAB23563	Aab23563 Human sod
73	14	50.0	1980	5	AAO14927	Aao14927 Human sod
74	14	50.0	1980	7	ADB78600	Adb78600 Human sod
75	14	50.0	1980	7	ADB78606	Adb78606 Human sod
76	14	50.0	1988	2	AAW69362	Aaw69362 Tetrodoto
77	13	46.4	521	2	AAW21738	Aaw21738 Variant r
78	13	46.4	1765	2	AAY16572	Aay16572 Type 5 so
79	13	46.4	1765	2	AAY41668	Aay41668 Rat senso
80	13	46.4	1765	2	AAY06597	Aay06597 Mouse sod
81	13	46.4	1765	2	AAY06596	Aay06596 Rat sodiu
82	13	46.4	1765	4	AAB20124	Aab20124 Mouse sod
83	13	46.4	1765	4	AAB20122	Aab20122 Rat sodiu
84	13	46.4	1765	4	AAB20123	Aab20123 Rat sodiu
85	13	46.4	1765	7	ADD32192	Add32192 Rat Na v
86	13	46.4	1765	7	ADD32210	Add32210 Rat Na v
87	13	46.4	1765	7	ADD32196	Add32196 Mouse Na
88	13	46.4	1765	7	ADE55104	Ade55104 Rat Prote
89	13	46.4	1791	4	AAB20121	Aab20121 Human sod
90	13	46.4	1791	5	AAO14925	Aao14925 Human sod
91	13	46.4	1791	7	ADD32194	Add32194 Human Na
92	13	46.4	1956	4	AAG65783	Aag65783 Rat SNS1
93	13	46.4	1956	4	AAG65785	Aag65785 Human SNS
94	13	46.4	1956	4	AAB61995	Aab61995 Rat perip
95	13	46.4	1956	4	AAB61996	Aab61996 Human per
96	13	46.4	1956	6	ABG76193	Abg76193 Human vol
97	13	46.4	1956	6	ABG75944	Abg75944 Rat perip
98	13	46.4	1956	6	ABG75945	Abg75945 Human per

99	13	46.4	1956	6	ABP72253	Abp72253 Human PN3
100	13	46.4	1956	6	ADA50144	Ada50144 Rat perip

ALIGNMENTS

RESULT 1
AAM15136
ID AAM15136 standard; protein; 405 AA.
XX
AC AAM15136;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #1570 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000670.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX
PS Claim 27; SEQ ID NO 19962; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 405 AA;

Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFPFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 158 GIFPFVSYIIISFLVVVNMYIAVILENF 185

RESULT 2
ABB34128
ID ABB34128 standard; peptide; 405 AA.
XX
AC ABB34128;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #1634 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 26763; 639pp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 405 AA;

Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFPFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 158 GIFPFVSYIIISFLVVVNMYIAVILENF 185

RESULT 3
AAM27591
ID AAM27591 standard; protein; 405 AA.
XX
AC AAM27591;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #1628 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.

XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 27860; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 405 AA;

Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 158 GIFFFVSYIIISFLVVVNMYIAVILENF 185

RESULT 4
ABB28960
ID ABB28960 standard; peptide; 405 AA.
XX
AC ABB28960;
XX
DT 01-FEB-2002 (first entry)
XX
DE Peptide #1611 encoded by breast cell single exon nucleic acid probe.
XX
KW Human; microarray; single exon probe; gene expression; breast; disease;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000662.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes, useful
PT for measuring gene expression in sample derived from human breast,
PT comprises number of single exon nucleic acid probes.
XX
PS Claim 27; SEQ ID NO 11928; 327pp + Sequence Listing; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting the
CC probes with a collection of detectably labelled nucleic acids derived
CC from mRNA of human breast, and then measuring the label bound to each
CC probe of the microarray. The probes are useful for verifying the
CC expression of regions of genomic DNA predicted to encode proteins. They
CC are useful for gene discovery, and for determining predisposition and/or
CC prognosing breast disease. Gene expression analysis is useful for
CC assessing the toxicity of chemical agents on cells. The microarray of
CC this invention presents a far greater diversity of probes for measuring
CC gene expression, with far less bias than expressed sequence tag
CC microarrays. The method is suitable for rapid production of functional
CC information from genomic sequence. The present sequence is a peptide
CC encoded by a single exon nucleic acid probe of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 405 AA;

Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 158 GIFFFVSYIIISFLVVVNMYIAVILENF 185

RESULT 5
ABB19569
ID ABB19569 standard; protein; 405 AA.
XX
AC ABB19569;
XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #1568 encoded by probe for measuring heart cell gene expression.
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.

```
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   hearts.
XX
PS   Claim 15; SEQ ID NO 21339; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart (see
CC   ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC   probe. The probes may be used for predicting, measuring and displaying
CC   gene expression in samples derived from the human heart via microarrays.
CC   By measuring gene expression, the probes are useful for predicting,
CC   diagnosing, grading, staging, monitoring and prognosing diseases of the
CC   human heart and vascular system e.g. cardiovascular disease,
CC   hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 405 AA;

  Query Match             100.0%;  Score 28;  DB 4;  Length 405;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db        158 GIFFFVSYIIISFLVVVNMYIAVILENF 185


RESULT 6
AAM67299
ID   AAM67299 standard; protein; 405 AA.
XX
AC   AAM67299;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 27605.
XX
KW   Human; bone marrow expressed exon; gene expression analysis; probe;
KW   microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS   Homo sapiens.
XX
PN   WO200157276-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000668.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488900/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human bone marrow.
XX
PS   Example 4; SEQ ID NO 27605; 658pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   bone marrow. They can be used to measure gene expression in bone marrow
CC   samples, which may enable the improved diagnosis and treatment of cancers
CC   such as lymphoma, leukaemia and myeloma. The present sequence is a
CC   protein encoded by one of the probes of the invention
XX
SQ   Sequence 405 AA;

  Query Match             100.0%;  Score 28;  DB 4;  Length 405;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db        158 GIFFFVSYIIISFLVVVNMYIAVILENF 185


RESULT 7
AAM54918
ID   AAM54918 standard; protein; 405 AA.
XX
AC   AAM54918;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 27023.
XX
KW   Human; brain expressed exon; gene expression analysis; probe; microarray;
KW   Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000667.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483446/52.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   brains.
XX
PS   Example 4; SEQ ID NO 27023; 650pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   brain. They can be used to measure gene expression in brain cell samples,
CC   which may enable the diagnosis and improved treatment of nervous system
CC   diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC   epilepsy and cancers. The present sequence is a protein encoded by one of
CC   the probes of the invention
XX
SQ   Sequence 405 AA;

  Query Match             100.0%;  Score 28;  DB 4;  Length 405;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db        158 GIFFFVSYIIISFLVVVNMYIAVILENF 185
```

RESULT 8
AAM56160
ID AAM56160 standard; protein; 405 AA.
XX
AC AAM56160;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28265.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
PS Example 4; SEQ ID NO 28265; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
SQ Sequence 405 AA;

Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 158 GIFFFVSYIIISFLVVVNMYIAVILENF 185

RESULT 9
ABG48961
ID ABG48961 standard; peptide; 405 AA.
XX
AC ABG48961;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID No 27609.
XX
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488898/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
PS Claim 27; SEQ ID NO 27609; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 405 AA;

Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 158 GIFFFVSYIIISFLVVVNMYIAVILENF 185

RESULT 10
AAM02877
ID AAM02877 standard; protein; 405 AA.
XX
AC AAM02877;
XX
DT 09-OCT-2001 (first entry)
XX
DE Peptide #1559 encoded by probe for measuring breast gene expression.
XX
KW Probe; human; breast disease; breast cancer; development disorder;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
PN WO200157270-A2.
XX
PD 09-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US000661.

```
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-476286/51.
XX
PT   Novel single exon nucleic acid probe used to measuring gene expression in
PT   a human breast.
XX
PS   Claim 27; SEQ ID NO 11617; 322pp; English.
XX
CC   The present invention relates to novel single exon nucleic acid probes
CC   (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
CC   such probe. The probes are useful for measuring human gene expression in
CC   a human breast sample, where the probe hybridises at high stringency to a
CC   nucleic acid expressed in the human breast. The probes are useful for
CC   predicting, diagnosing, grading, staging, monitoring and prognosing
CC   diseases of the human breast, particularly those diseases with polygenic
CC   aetiology. The diseases include: breast cancer, disorders of development,
CC   inflammatory diseases of the breast, fibrocystic changes, proliferative
CC   breast disease and non-carcinoma tumours. Note: The sequence data for
CC   this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 405 AA;

  Query Match             100.0%;  Score 28;  DB 4;  Length 405;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db        158 GIFFFVSYIIISFLVVVNMYIAVILENF 185


RESULT 11
AAM04075
ID   AAM04075 standard; protein; 405 AA.
XX
AC   AAM04075;
XX
DT   09-OCT-2001  (first entry)
XX
DE   Peptide #2757 encoded by probe for measuring breast gene expression.
XX
KW   Probe; human; breast disease; breast cancer; development disorder;
KW   inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS   Homo sapiens.
XX
PN   WO200157270-A2.
XX
PD   09-AUG-2001.
XX
PF   29-JAN-2001; 2001WO-US000661.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-476286/51.
XX
PT   Novel single exon nucleic acid probe used to measuring gene expression in
PT   a human breast.
XX
PS   Claim 27; SEQ ID NO 12815; 322pp; English.
XX
CC   The present invention relates to novel single exon nucleic acid probes
CC   (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
CC   such probe. The probes are useful for measuring human gene expression in
CC   a human breast sample, where the probe hybridises at high stringency to a
CC   nucleic acid expressed in the human breast. The probes are useful for
CC   predicting, diagnosing, grading, staging, monitoring and prognosing
CC   diseases of the human breast, particularly those diseases with polygenic
CC   aetiology. The diseases include: breast cancer, disorders of development,
CC   inflammatory diseases of the breast, fibrocystic changes, proliferative
CC   breast disease and non-carcinoma tumours. Note: The sequence data for
CC   this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 405 AA;

  Query Match             100.0%;  Score 28;  DB 4;  Length 405;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db        158 GIFFFVSYIIISFLVVVNMYIAVILENF 185


RESULT 12
ABG36946
ID   ABG36946 standard; peptide; 405 AA.
XX
AC   ABG36946;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human peptide encoded by genome-derived single exon probe SEQ ID 26611.
XX
KW   Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW   chronic obstructive pulmonary disease; interstitial lung disease;
KW   familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW   tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW   Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW   pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
KW   primary ciliary dyskinesis; pulmonary hypertension;
KW   hyaline membrane disease.
XX
OS   Homo sapiens.
XX
PN   WO200186003-A2.
XX
PD   15-NOV-2001.
XX
PF   30-JAN-2001; 2001WO-US000665.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
```

PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
PS Claim 27; SEQ ID NO 26611; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC ; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesis, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 405 AA;

Query Match 100.0%; Score 28; DB 5; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 158 GIFFFVSYIIISFLVVVNMYIAVILENF 185

RESULT 13
ADB78597
ID ADB78597 standard; protein; 1855 AA.
XX
AC ADB78597;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:141.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78636.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 141; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 1855 AA;

Query Match 100.0%; Score 28; DB 7; Length 1855;
Best Local Similarity 100.0%; Pred. No. 1e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 1762 GIFFFVSYIIISFLVVVNMYIAVILENF 1789

RESULT 14
ADB78607
ID ADB78607 standard; protein; 1950 AA.

XX
AC ADB78607;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:151.
XX
KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78646.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 151; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 1950 AA;

Query Match 100.0%; Score 28; DB 7; Length 1950;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 1697 GIFFFVSYIIISFLVVVNMYIAVILENF 1724

RESULT 15
ADE59628
ID ADE59628 standard; protein; 1951 AA.
XX
AC ADE59628;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein NP_037251, SEQ ID NO 5524.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; NP_037251.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1951 AA;

```
  Query Match             100.0%;  Score 28;  DB 7;  Length 1951;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1698 GIFFFVSYIIISFLVVVNMYIAVILENF 1725


RESULT 16
ADL06576
ID   ADL06576 standard; protein; 1951 AA.
XX
AC   ADL06576;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human tumour-associated antigenic target (TAT) polypeptide #75.
XX
KW   Human; tumour-associated antigenic target; TAT; cell death; tumour;
KW   cancer; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2004016225-A2.
XX
PD   26-FEB-2004.
XX
PF   19-AUG-2003; 2003WO-US025892.
XX
PR   19-AUG-2002; 2002US-0404809P.
PR   21-AUG-2002; 2002US-0405645P.
PR   23-SEP-2002; 2002US-0413192P.
PR   15-OCT-2002; 2002US-0419008P.
PR   15-NOV-2002; 2002US-0426847P.
PR   02-JUL-2003; 2003US-0484959P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Desauvage FJ,  Frantz G,  Hillan KJ,  Polakis P,  Polson A,  Smith V;
PI   Spencer SD,  Wu TD,  Zhang Z;
XX
DR   WPI; 2004-257144/24.
DR   N-PSDB; ADL06499.
XX
PT   New antibody that binds to a tumor-associated antigenic target (TAT)
PT   polypeptide, useful for preparing a composition for diagnosing or
PT   treating cancer.
XX
PS   Claim 2; SEQ ID NO 156; 319pp; English.
XX
CC   The present invention relates to the isolation of human tumour-associated
CC   antigenic target (TAT) polynucleotide and polypeptide sequences. Also
CC   disclosed is an antibody that binds to a TAT polypeptide. The antibody is
CC   a monoclonal antibody, an antibody fragment, a chimeric antibody or a
CC   humanised antibody. It is conjugated to a growth inhibitory agent. It is
CC   produced in bacteria or in CHO cells and induces death of a cell to which
CC   it binds. The antibody is useful for preparing a composition for
CC   diagnosing or treating tumours and cancer. The present sequence
CC   represents a human TAT polypeptide of the invention.
XX
SQ   Sequence 1951 AA;

  Query Match             100.0%;  Score 28;  DB 8;  Length 1951;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1698 GIFFFVSYIIISFLVVVNMYIAVILENF 1725


RESULT 17
AAE20511
ID   AAE20511 standard; protein; 1962 AA.
XX
AC   AAE20511;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel protein #2.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   medical disorder.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 981
FT                   /note= "Encoded by MTG"
FT   Misc-difference 1056
FT                   /note= "Encoded by RCA"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US025650.
XX
PR   16-AUG-2000; 2000US-0225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   N-PSDB; AAD32840.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders.
XX
PS   Claim 1; Page 37-41; 83pp; English.
XX
CC   The present sequence is novel human protein (NHP), ion channel protein.
CC   NHP share structural similarity with mammalian sodium channel proteins
CC   particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC   are useful as hybridisation probes for screening libraries and assessing
CC   gene expression patterns. Sequences derived from regions adjacent to the
CC   intron/exon boundaries of NHP gene can be used to design primers for use
CC   in amplification assays to detect mutations within the exons, splice
CC   sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC   nucleotide sequences are useful for drug screening effective in the
CC   treatment of symptomatic or phenotypic manifestations of perturbing the
CC   normal function of NHP in the body, and nucleotide constructs encoding
CC   NHP products are useful to genetically engineer host cells to express NHP
CC   products in vivo. These genetically engineered cells function as
CC   bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC   peptide, or a NHP fusion protein to the body. Nucleotide construct
CC   encoding NHP products are also useful in gene therapy for modulating NHP
CC   expression and to produce genetically engineered host cells to express
CC   NHP products in vivo. NHP nucleotide sequences may also be used as part
CC   of ribozyme and/or triple helix sequences that are useful for NHP gene
CC   regulation. The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases
XX
SQ   Sequence 1962 AA;

  Query Match             100.0%;  Score 28;  DB 5;  Length 1962;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1751 GIFFFVSYIIISFLVVVNMYIAVILENF 1778
```

RESULT 18
AAE20516
ID AAE20516 standard; protein; 1973 AA.
XX
AC AAE20516;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel protein #7.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW medical disorder.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Misc-difference 992
FT   /note= "Encoded by MTG"
FT Misc-difference 1067
FT   /note= "Encoded by RCA"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025650.
XX
PR 16-AUG-2000; 2000US-0225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR N-PSDB; AAD32845.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
PS Claim 1; Page 64-68; 83pp; English.
XX
CC The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins
CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the
CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or triple helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
SQ Sequence 1973 AA;

```
  Query Match             100.0%;  Score 28;  DB 5;  Length 1973;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1762 GIFFFVSYIIISFLVVVNMYIAVILENF 1789
```

RESULT 19
ABR83185
ID ABR83185 standard; protein; 1981 AA.
XX
AC ABR83185;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human SCN1A splice variant -84P:SCN1ADELp654-681.
XX
KW SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
KW neuroprotective; anesthetic; cytostatic; cerebroprotective; cardiant;
KW hypotensive; gene therapy; human; splice variant.
XX
OS Homo sapiens.
XX
PN WO2003072751-A2.
XX
PD 04-SEP-2003.
XX
PF 25-FEB-2003; 2003WO-US006010.
XX
PR 25-FEB-2002; 2002US-0359382P.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI George AL, Lossin C;
XX
DR WPI; 2003-712725/67.
DR N-PSDB; ACF57880.
XX
PT Recombinantly expressed sodium channel type 1 alpha subunit, useful in
PT screening for modulators, for treating e.g. epilepsy.
XX
PS Disclosure; Page 162-169; 176pp; English.
XX
CC The invention relates to a recombinantly expressed and isolated human
CC SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
CC incorporated into a cell, is used to screen for specific modulators,
CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,
CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
CC motor endplate diseases, hypertension, congestive heart failure and
CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
CC and metastatic cancer cell lines). These activities can also be provided
CC by gene therapy vectors that express (I) or the modulators. The
CC modulators, also antibodies directed against (I), are used to detect
CC sodium channel polypeptides. The present sequence represents a human
CC SCN1A splice variant 84P:SCN1ADELp654-681
XX
SQ Sequence 1981 AA;

```
  Query Match             100.0%;  Score 28;  DB 7;  Length 1981;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1734 GIFFFVSYIIISFLVVVNMYIAVILENF 1761
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```
RESULT 20
AAE20510
ID   AAE20510 standard; protein; 1998 AA.
XX
AC   AAE20510;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel protein #1.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   medical disorder.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 981
FT                   /note= "Encoded by MTG"
FT   Misc-difference 1056
FT                   /note= "Encoded by RCA"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US025650.
XX
PR   16-AUG-2000; 2000US-0225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   N-PSDB; AAD32839.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders.
XX
PS   Claim 1; Page 30-34; 83pp; English.
XX
CC   The present sequence is novel human protein (NHP), ion channel protein.
CC   NHP share structural similarity with mammalian sodium channel proteins
CC   particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC   are useful as hybridisation probes for screening libraries and assessing
CC   gene expression patterns. Sequences derived from regions adjacent to the
CC   intron/exon boundaries of NHP gene can be used to design primers for use
CC   in amplification assays to detect mutations within the exons, splice
CC   sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC   nucleotide sequences are useful for drug screening effective in the
CC   treatment of symptomatic or phenotypic manifestations of perturbing the
CC   normal function of NHP in the body, and nucleotide constructs encoding
CC   NHP products are useful to genetically engineer host cells to express NHP
CC   products in vivo. These genetically engineered cells function as
CC   bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC   peptide, or a NHP fusion protein to the body. Nucleotide construct
CC   encoding NHP products are also useful in gene therapy for modulating NHP
CC   expression and to produce genetically engineered host cells to express
CC   NHP products in vivo. NHP nucleotide sequences may also be used as part
CC   of ribozyme and/or triple helix sequences that are useful for NHP gene
CC   regulation. The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases
XX
SQ   Sequence 1998 AA;

  Query Match             100.0%;  Score 28;  DB 5;  Length 1998;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1751 GIFFFVSYIIISFLVVVNMYIAVILENF 1778


RESULT 21
ABR83184
ID   ABR83184 standard; protein; 1998 AA.
XX
AC   ABR83184;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human SCN1A splice variant -33P:SCN1ADELp671-681.
XX
KW   SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
KW   neuroprotective; anesthetic; cytostatic; cerebroprotective; cardiant;
KW   hypotensive; gene therapy; human; splice variant.
XX
OS   Homo sapiens.
XX
PN   WO2003072751-A2.
XX
PD   04-SEP-2003.
XX
PF   25-FEB-2003; 2003WO-US006010.
XX
PR   25-FEB-2002; 2002US-0359382P.
XX
PA   (UYVA-) UNIV VANDERBILT.
XX
PI   George AL,  Lossin C;
XX
DR   WPI; 2003-712725/67.
DR   N-PSDB; ACF57879.
XX
PT   Recombinantly expressed sodium channel type 1 alpha subunit, useful in
PT   screening for modulators, for treating e.g. epilepsy.
XX
PS   Disclosure; Page 148-156; 176pp; English.
XX
CC   The invention relates to a recombinantly expressed and isolated human
CC   SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
CC   incorporated into a cell, is used to screen for specific modulators,
CC   potentially useful as anticonvulsant, antiepileptic, neuroprotective,
CC   analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
CC   epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
CC   motor endplate diseases, hypertension, congestive heart failure and
CC   muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
CC   and metastatic cancer cell lines). These activities can also be provided
CC   by gene therapy vectors that express (I) or the modulators. The
CC   modulators, also antibodies directed against (I), are used to detect
CC   sodium channel polypeptides. The present sequence represents a human
CC   SCN1A splice variant 33P:SCN1ADELp671-681 encoding cDNA
XX
SQ   Sequence 1998 AA;

  Query Match             100.0%;  Score 28;  DB 7;  Length 1998;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1751 GIFFFVSYIIISFLVVVNMYIAVILENF 1778


RESULT 22
ABB06026
ID   ABB06026 standard; protein; 1999 AA.
XX
AC   ABB06026;
XX
```

DT 10-MAY-2002 (first entry)
XX
DE Human sodium channel SCN1A protein SEQ ID NO:2.
XX
KW Human; sodium channel; SCN1A; chromosome 2q24;
KW familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
OS Homo sapiens.
XX
PN WO200196552-A1.
XX
PD 20-DEC-2001.
XX
PF 12-JUN-2001; 2001WO-JP004956.
XX
PR 13-JUN-2000; 2000JP-00177540.
PR 13-JUN-2000; 2000JP-00177544.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Kanazawa I, Goto J, Jeong S;
XX
DR WPI; 2002-098066/13.
DR N-PSDB; ABL39689.
XX
PT Human sodium channels SCN1A and SCN3A and encoded genes, useful in
PT studying physiological mechanism in which excitant cells participate and
PT causes of diseases and developing drugs for motor endplate disease.
XX
PS Claim 1; Page 40-49; 88pp; Japanese.
XX
CC The present invention describes human sodium channels SCN1A and SCN3A.
CC The present sequence represents the human sodium channel SCN1A. SCN1A and
CC SCN3A have been located to the human chromosome 2 long arm, positions
CC 2q24 and 2q24-31 respectively. The sodium channel proteins are useful in
CC studying the physiological mechanism in which excitant cells participate
CC and cause human diseases, and in developing remedies for e.g. familial
CC hypercalcaemic periodic paralysis of extremities and motor endplate
CC disease
XX
SQ Sequence 1999 AA;

Query Match 100.0%; Score 28; DB 5; Length 1999;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 1752 GIFFFVSYIIISFLVVVNMYIAVILENF 1779

RESULT 23
ABB06027
ID ABB06027 standard; protein; 2000 AA.
XX
AC ABB06027;
XX
DT 10-MAY-2002 (first entry)
XX
DE Human sodium channel SCN3A protein SEQ ID NO:4.
XX
KW Human; sodium channel; SCN3A; chromosome 2q24-31;
KW familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
OS Homo sapiens.
XX
PN WO200196552-A1.
XX
PD 20-DEC-2001.
XX
PF 12-JUN-2001; 2001WO-JP004956.
XX
PR 13-JUN-2000; 2000JP-00177540.
PR 13-JUN-2000; 2000JP-00177544.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Kanazawa I, Goto J, Jeong S;
XX
DR WPI; 2002-098066/13.
DR N-PSDB; ABL39690.
XX
PT Human sodium channels SCN1A and SCN3A and encoded genes, useful in
PT studying physiological mechanism in which excitant cells participate and
PT causes of diseases and developing drugs for motor endplate disease.
XX
PS Claim 2; Page 72-81; 88pp; Japanese.
XX
CC The present invention describes human sodium channels SCN1A and SCN3A.
CC The present sequence represents the human sodium channel SCN3A. SCN1A and
CC SCN3A have been located to the human chromosome 2 long arm, positions
CC 2q24 and 2q24-31 respectively. The sodium channel proteins are useful in
CC studying the physiological mechanism in which excitant cells participate
CC and cause human diseases, and in developing remedies for e.g. familial
CC hypercalcaemic periodic paralysis of extremities and motor endplate
CC disease
XX
SQ Sequence 2000 AA;

Query Match 100.0%; Score 28; DB 5; Length 2000;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 1747 GIFFFVSYIIISFLVVVNMYIAVILENF 1774

RESULT 24
ADK81762
ID ADK81762 standard; protein; 2000 AA.
XX
AC ADK81762;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human Nav1.3 protein.
XX
KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia.
XX
OS Homo sapiens.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberds SL;
XX
DR WPI; 2004-203785/19.
DR N-PSDB; ADK81761.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Disclosure; SEQ ID NO 9096; 417pp; English.
XX

CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents human Nav1.3 protein.
XX
SQ Sequence 2000 AA;

Query Match 100.0%; Score 28; DB 8; Length 2000;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 1747 GIFFFVSYIIISFLVVVNMYIAVILENF 1774

RESULT 25
AAB99676
ID AAB99676 standard; protein; 2005 AA.
XX
AC AAB99676;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human adult form of SCN2A protein sequence SEQ ID NO:35.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA001404.
XX
PR 26-NOV-1999; 99US-0167623P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR N-PSDB; AAH55793.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
PS Disclosure; Page 123-130; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 4; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 1752 GIFFFVSYIIISFLVVVNMYIAVILENF 1779

Search completed: January 27, 2005, 17:45:18
Job time : 88.5 secs

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:36:05 ; Search time 17 Seconds
(without alignments)
158.475 Million cell updates/sec

Title: US-10-608-584-29
Perfect score: 28
Sequence: 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	100.0	303	2	S29185	sodium channel pro
2	28	100.0	423	2	S29184	sodium channel pro
3	28	100.0	1951	2	S00320	sodium channel pro
4	28	100.0	1983	2	A60054	sodium channel pro
5	28	100.0	2005	2	B25019	sodium channel pro
6	28	100.0	2009	2	A25019	sodium channel pro
7	24	85.7	1977	2	S54771	sodium channel alp
8	20	71.4	70	2	I59194	sodium channel pro
9	17	60.7	1993	2	T30902	sodium channel SCA
10	16	57.1	2005	2	A46269	sodium channel alp
11	14	50.0	324	2	A45752	sodium channel pro
12	14	50.0	1976	2	I56555	sodium channel pro
13	13	46.4	1765	2	T42388	sodium channel alp
14	13	46.4	1957	2	S68453	sodium channel pro
15	12	42.9	1699	2	T31340	voltage-gated sodi
16	11	39.3	1522	2	JC1101	sodium channel pro
17	11	39.3	1695	2	JE0084	voltage-gated sodi
18	11	39.3	1739	2	A48298	sodium channel hom
19	11	39.3	1784	2	T43167	sodium channel pro
20	11	39.3	1820	1	CHEE	sodium channel pro
21	10	35.7	213	2	A30302	sodium channel pro
22	10	35.7	428	2	S35215	sodium channel pro
23	10	35.7	1689	2	S72467	sodium channel pro
24	10	35.7	1820	2	A33299	sodium channel pro
25	10	35.7	2108	2	S72458	sodium channel pro
26	8	28.6	1835	2	I54323	sodium channel alp
27	8	28.6	1836	2	I64893	sodium channel alp
28	8	28.6	1836	2	JS0648	sodium channel alp
29	8	28.6	1836	2	I51964	sodium channel alp
30	8	28.6	1840	1	CHRTM1	sodium channel pro
31	7	25.0	79	2	G82709	hypothetical prote
32	7	25.0	675	2	B75036	hypothetical prote
33	7	25.0	2016	2	A38195	sodium channel pro
34	7	25.0	2019	2	A33996	sodium channel pro
35	7	25.0	2049	2	T43161	sodium channel pro
36	6	21.4	20	2	T26748	hypothetical prote
37	6	21.4	77	2	D64041	hypothetical prote
38	6	21.4	88	2	T17785	hypothetical prote
39	6	21.4	120	2	S62764	NADH2 dehydrogenas
40	6	21.4	122	2	F71180	hypothetical prote
41	6	21.4	161	2	B96537	hypothetical prote
42	6	21.4	171	2	S55958	probable membrane
43	6	21.4	181	2	A87367	transcription regu
44	6	21.4	197	2	D86856	hypothetical prote
45	6	21.4	206	2	B71821	hypothetical prote
46	6	21.4	206	2	T01312	hypothetical prote
47	6	21.4	226	2	G95247	hypothetical prote
48	6	21.4	231	2	S12124	probable heme-bind
49	6	21.4	246	2	D98112	hypothetical prote
50	6	21.4	259	2	AI3223	hypothetical prote
51	6	21.4	262	2	S59078	conserved hypothet
52	6	21.4	269	2	F97327	nitroreductase fam
53	6	21.4	274	2	I50682	tenascin - chicken
54	6	21.4	277	2	E75187	sugar abc transpor
55	6	21.4	317	2	B83039	probable permease
56	6	21.4	317	2	H97240	amino acid transpo
57	6	21.4	331	2	H98020	hypothetical prote
58	6	21.4	341	2	T28798	hypothetical prote
59	6	21.4	341	2	E83737	C4-dicarboxylate t
60	6	21.4	370	1	XNVKUD	UDPglucose-hexose-
61	6	21.4	371	2	S75778	oligopeptide trans
62	6	21.4	374	2	T25943	hypothetical prote
63	6	21.4	380	2	T11114	ubiquinol-cytochro
64	6	21.4	399	2	T21015	hypothetical prote
65	6	21.4	419	2	T07817	S-locus-specific g
66	6	21.4	431	2	AF1422	cellobiose phospho
67	6	21.4	444	2	I40417	glycerol-3-phospha
68	6	21.4	463	2	E81141	xanthine/uracil pe
69	6	21.4	465	2	C86911	probable cell-divi
70	6	21.4	465	2	T10012	probable cell divi
71	6	21.4	469	2	G70699	probable rodA prot
72	6	21.4	487	2	T27069	hypothetical prote
73	6	21.4	490	2	T32003	hypothetical prote
74	6	21.4	506	2	T23163	hypothetical prote
75	6	21.4	515	2	T03717	GTP-binding protei
76	6	21.4	533	2	AB0146	probable Branched-
77	6	21.4	545	2	S59143	NADH2 dehydrogenas
78	6	21.4	545	2	T01288	protein kinase F27
79	6	21.4	558	2	E70756	hypothetical glyci
80	6	21.4	589	2	H69691	two-component sens
81	6	21.4	627	2	S67257	proline transport
82	6	21.4	634	2	T33528	hypothetical prote
83	6	21.4	666	2	F90069	hypothetical prote
84	6	21.4	710	2	T00055	hypothetical prote
85	6	21.4	713	2	A81317	probable integral
86	6	21.4	862	2	C97343	hypothetical prote
87	6	21.4	939	2	S75908	hypothetical prote
88	6	21.4	1195	2	C87691	hypothetical prote
89	6	21.4	1341	2	T18301	latrophilin-2, spl
90	6	21.4	1354	2	T18375	latrophilin-2 (spl
91	6	21.4	1356	2	T18367	latrophilin-2, spl
92	6	21.4	1369	2	T18379	latrophilin-2 (spl
93	6	21.4	1384	2	T18366	latrophilin-2, spl
94	6	21.4	1397	2	T18377	latrophilin-2 (spl
95	6	21.4	1399	2	T18370	latrophilin-2 (spl
96	6	21.4	1407	2	T18381	latrophilin-2 (spl
97	6	21.4	1412	2	T18380	latrophilin-2 (spl
98	6	21.4	1420	2	T18385	latrophilin-2 (spl
99	6	21.4	1422	2	T18383	latrophilin-2, spl
100	6	21.4	1435	2	T18387	latrophilin-2 (spl

ALIGNMENTS

RESULT 1
S29185
sodium channel protein II - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Aug-1999
C;Accession: S29185; S34777
R;Lu, C.M.; Han, J.; Rado, T.A.; Brown, G.B.
FEBS Lett. 303, 53-58, 1992
A;Title: Differential expression of two sodium channel subtypes in human brain.
A;Reference number: S29184; MUID:92275082; PMID:1317301
A;Accession: S29185
A;Molecule type: mRNA
A;Residues: 1-303 <LUC>
A;Cross-references: EMBL:X65361
R;Lu, C.; Han, J.; Rado, T.A.; Brown, G.B.
submitted to the EMBL Data Library, April 1992
A;Reference number: S34777
A;Accession: S34777
A;Molecule type: mRNA
A;Residues: 8-251,'N' <LU2>
A;Cross-references: EMBL:X65361; NID:g36419; PIDN:CAA46438.1; PID:g36420
C;Superfamily: sodium channel protein
C;Keywords: duplication; sodium channel; transmembrane protein; voltage-gated ion channe
F;51-75/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 28; DB 2; Length 303;
Best Local Similarity 100.0%; Pred. No. 6.9e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 51 GIFFFVSYIIISFLVVVNMYIAVILENF 78

RESULT 2
S29184
sodium channel protein I - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S29184
R;Lu, C.M.; Han, J.; Rado, T.A.; Brown, G.B.
FEBS Lett. 303, 53-58, 1992
A;Title: Differential expression of two sodium channel subtypes in human brain.
A;Reference number: S29184; MUID:92275082; PMID:1317301
A;Accession: S29184
A;Molecule type: mRNA
A;Residues: 1-423 <LUC>
A;Cross-references: UNIPROT:P35498; EMBL:X65362; NID:g36417; PIDN:CAA46439.1; PID:g36418
C;Genetics:
A;Map position: 2q23-q24
C;Superfamily: sodium channel protein
C;Keywords: duplication; sodium channel; transmembrane protein; voltage-gated ion channe
F;20-43/Domain: transmembrane #status predicted <TM1>
F;55-78/Domain: transmembrane #status predicted <TM2>
F;85-108/Domain: transmembrane #status predicted <TM3>
F;120-139/Domain: transmembrane #status predicted <TM4>
F;156-178/Domain: transmembrane #status predicted <TM5>
F;245-269/Domain: transmembrane #status predicted <TM6>

Query Match 100.0%; Score 28; DB 2; Length 423;
Best Local Similarity 100.0%; Pred. No. 9e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 245 GIFFFVSYIIISFLVVVNMYIAVILENF 272

RESULT 3
S00320
sodium channel protein III - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S00320
R;Kayano, T.; Noda, M.; Flockerzi, V.; Takahashi, H.; Numa, S.
FEBS Lett. 228, 187-194, 1988
A;Title: Primary structure of rat brain sodium channel III deduced from the cDNA sequ
A;Reference number: S00320; MUID:88137594; PMID:2449363
A;Accession: S00320
A;Molecule type: mRNA
A;Residues: 1-1951 <KAY>
A;Cross-references: UNIPROT:P08104; EMBL:Y00766; NID:g57210; PIDN:CAA68735.1; PID:g572
A;Note: 270-Ile, 278-Leu, 355-Thr, 513-Lys, and 1059-Arg were also found
C;Superfamily: sodium channel protein
C;Keywords: duplication; transmembrane protein

Query Match 100.0%; Score 28; DB 2; Length 1951;
Best Local Similarity 100.0%; Pred. No. 3.2e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 1698 GIFFFVSYIIISFLVVVNMYIAVILENF 1725

RESULT 4
A60054
sodium channel protein IIIb, long form - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60054; B44824
R;Joho, R.H.; Moorman, J.R.; VanDongen, A.M.J.; Kirsch, G.E.; Silberberg, H.; Schuster,
Brain Res. Mol. Brain Res. 7, 105-113, 1990
A;Title: Toxin and kinetic profile of rat brain type III sodium channels expressed in X
A;Reference number: A60054; MUID:90251117; PMID:2160038
A;Accession: A60054
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1983 <JOH>
A;Cross-references: UNIPROT:Q64243
R;Schaller, K.L.; Krzemien, D.M.; McKenna, N.M.; Caldwell, J.H.
J. Neurosci. 12, 1370-1381, 1992
A;Title: Alternatively spliced sodium channel transcripts in brain and muscle.
A;Reference number: A44824; MUID:92211397; PMID:1313493
A;Accession: B44824
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 611-662 <SCH>
A;Cross-references: GB:S97388; NID:g248225; PIDN:AAB21984.1; PID:g248226
A;Experimental source: skeletal muscle
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:97388, NCBIP:97391)
C;Superfamily: sodium channel protein
C;Keywords: duplication; glycoprotein; ion transport; sodium channel; transmembrane prot

Query Match 100.0%; Score 28; DB 2; Length 1983;
Best Local Similarity 100.0%; Pred. No. 3.2e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 1730 GIFFFVSYIIISFLVVVNMYIAVILENF 1757

RESULT 5
B25019
sodium channel protein II - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: B25019; S24804
R;Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H
Nature 320, 188-192, 1986
A;Title: Existence of distinct sodium channel messenger RNAs in rat brain.

A;Reference number: A93377; MUID:86146901; PMID:3754035
A;Accession: B25019
A;Molecule type: mRNA
A;Residues: 1-2005 <NOD>
A;Cross-references: UNIPROT:Q63509
A;Experimental source: brain
R;Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
submitted to the EMBL Data Library, August 1991
A;Description: Developmentally regulated RNA splicing of rat brain sodium channel mRNAs.
A;Reference number: S24803
A;Accession: S24804
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 183-188,'D',190-305 <SAR>
A;Cross-references: EMBL:X61149; NID:g57074; PIDN:CAA43458.1; PID:g57076
C;Superfamily: sodium channel protein
C;Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-g

Query Match 100.0%; Score 28; DB 2; Length 2005;
Best Local Similarity 100.0%; Pred. No. 3.2e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 1752 GIFFFVSYIIISFLVVVNMYIAVILENF 1779

RESULT 6
A25019
sodium channel protein I - rat
N;Alternate names: sodium channel protein A
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A25019; S40783; I84764
R;Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H
Nature 320, 188-192, 1986
A;Title: Existence of distinct sodium channel messenger RNAs in rat brain.
A;Reference number: A93377; MUID:86146901; PMID:3754035
A;Accession: A25019
A;Molecule type: mRNA
A;Residues: 1-2009 <NOD>
A;Cross-references: UNIPROT:P04774; GB:X03638; NID:g57216; PIDN:CAA27286.1; PID:g57217
A;Experimental source: brain
R;Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
Nucleic Acids Res. 19, 5673-5679, 1991
A;Title: Developmentally regulated alternative RNA splicing of rat brain sodium channel
A;Reference number: S40782; MUID:92051314; PMID:1658739
A;Accession: S40783
A;Molecule type: DNA
A;Residues: 177-253 <SAR>
R;Noda, M.; Numa, S.
J. Recept. Res. 7, 467-497, 1987
A;Title: Structure and function of sodium channel.
A;Reference number: I50536; MUID:87311395; PMID:2442385
A;Accession: I84764
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2009 <RES>
A;Cross-references: GB:M22253; NID:g1041088; PIDN:AAA79965.1; PID:g1041089
C;Superfamily: sodium channel protein
C;Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-g

Query Match 100.0%; Score 28; DB 2; Length 2009;
Best Local Similarity 100.0%; Pred. No. 3.2e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||||||
Db 1762 GIFFFVSYIIISFLVVVNMYIAVILENF 1789

RESULT 7
S54771
sodium channel alpha subunit - human
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54771
R;Klugbauer, N.; Lacinova, L.; Flockerzi, V.; Hofmann, F.
EMBO J. 14, 1084-1090, 1995
A;Title: Structure and functional expression of a new member of the tetrodotoxin-sensiti
A;Reference number: S54771; MUID:95237189; PMID:7720699
A;Accession: S54771
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1977 <KLU>
A;Cross-references: UNIPROT:Q15858; EMBL:X82835; NID:g758109; PIDN:CAA58042.1; PID:g7581
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 85.7%; Score 24; DB 2; Length 1977;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FVSYIIISFLVVVNMYIAVILENF 28
||||||||||||||||||||||||
Db 1729 FVSYIIISFLVVVNMYIAVILENF 1752

RESULT 8
I59194
sodium channel protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Nov-1997
C;Accession: I59194
R;Han, J.; Lu, C.
Proc. Natl. Acad. Sci. U.S.A. 88, 335-339, 1991
A;Title: Direct amplification of a single dissected chromosomal segment by polymerase ch
A;Reference number: I59194; MUID:91110524; PMID:1846440
A;Accession: I59194
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-70 <RES>
A;Cross-references: GB:M55662; NID:g179560; PID:g553206
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 71.4%; Score 20; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLVVVNMY 20
||||||||||||||||||||
Db 51 GIFFFVSYIIISFLVVVNMY 70

RESULT 9
T30902
sodium channel SCAP1 alpha chain - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30902
R;Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.
DNA Cell Biol. 16, 347-356, 1997
A;Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit cDNA.
A;Reference number: Z20929; MUID:97238630; PMID:9115644
A;Accession: T30902
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1993 <DYE>
A;Cross-references: UNIPROT:P90670; EMBL:U66915; NID:g1842248; PID:g1842249; PIDN:AAC474
C;Superfamily: sodium channel protein

Query Match 60.7%; Score 17; DB 2; Length 1993;
Best Local Similarity 100.0%; Pred. No. 3.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          12 SFLVVVNMYIAVILENF 28
               |||||||||||||||||
Db        1719 SFLVVVNMYIAVILENF 1735
```

RESULT 10
A46269
sodium channel alpha chain HBA - human
C;Species: Homo sapiens (man)
C;Date: 20-Oct-1993 #sequence_revision 18-Nov-1994 #text_change 21-Nov-1997
C;Accession: A46269
R;Ahmed, C.M.; Ware, D.H.; Lee, S.C.; Patten, C.D.; Ferrer-Montiel, A.V.; Schinder, A.F.
Proc. Natl. Acad. Sci. U.S.A. 89, 8220-8224, 1992
A;Title: Primary structure, chromosomal localization, and functional expression of a vol
A;Reference number: A46269; MUID:92390418; PMID:1325650
A;Accession: A46269
A;Molecule type: mRNA
A;Residues: 1-2005 <AHM>
A;Cross-references: GB:M94055
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:113082)
C;Genetics:
A;Map position: 2q23-q24.3
C;Superfamily: sodium channel protein
C;Keywords: duplication

```
  Query Match             57.1%;  Score 16;  DB 2;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 GIFFFVSYIIISFLVV 16
               ||||||||||||||||
Db        1752 GIFFFVSYIIISFLVV 1767
```

RESULT 11
A45752
sodium channel protein pCSC-1 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
C;Accession: A45752
R;Sills, M.N.; Xu, Y.C.; Baracchini, E.; Goodman, R.H.; Cooperman, S.S.; Mandel, G.; Chi
J. Clin. Invest. 84, 331-336, 1989
A;Title: Expression of diverse Na(+) channel messenger RNAs in rat myocardium. Evidence
A;Reference number: A45752; MUID:89292178; PMID:2544627
A;Accession: A45752
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-324 <SIL>
A;Cross-references: UNIPROT:Q63360; GB:M27223; NID:g205611; PIDN:AAA41666.1; PID:g205612
C;Superfamily: sodium channel protein
C;Keywords: duplication

```
  Query Match             50.0%;  Score 14;  DB 2;  Length 324;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-07;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 GIFFFVSYIIISFL 14
               ||||||||||||||
Db          86 GIFFFVSYIIISFL 99
```

RESULT 12
I56555
sodium channel protein 6 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56555
R;Schaller, K.L.; Krzemien, D.M.; Yarowsky, P.J.; Krueger, B.K.; Caldwell, J.H.
J. Neurosci. 15, 3231-3242, 1995
A;Title: A novel, abundant sodium channel expressed in neurons and glia.
A;Reference number: I56555; MUID:95271284; PMID:7751906
A;Accession: I56555
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1976 <RES>
A;Cross-references: UNIPROT:Q63541; GB:L39018; NID:g829033; PIDN:AAC42059.1; PID:g829034
C;Genetics:
A;Gene: SCP6
C;Superfamily: sodium channel protein
C;Keywords: duplication

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  Query Match             50.0%;  Score 14;  DB 2;  Length 1976;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 GIFFFVSYIIISFL 14
               ||||||||||||||
Db        1738 GIFFFVSYIIISFL 1751
```

RESULT 13
T42388
sodium channel alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42388
R;Dib-Hajj, S.D.; Tyrrell, L.; Black, J.A.; Waxman, S.G.
Proc. Natl. Acad. Sci. U.S.A. 95, 8963-8968, 1998
A;Title: NaN, a novel voltage-gated Na channel, is expressed preferentially in periphera
A;Reference number: Z22149; MUID:98338024; PMID:9671787
A;Accession: T42388
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1765 <DIB>
A;Cross-references: UNIPROT:O88457; EMBL:AF059030; NID:g3372614; PID:g3372615; PIDN:AAC4
A;Experimental source: strain Sprague-Dawley; dorsal root ganglia
A;Note: preferentially expressed in sensory neurons within dorsal root ganglia and trige
C;Superfamily: sodium channel protein

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  Query Match             46.4%;  Score 13;  DB 2;  Length 1765;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          16 VVNMYIAVILENF 28
               |||||||||||||
Db        1575 VVNMYIAVILENF 1587
```

RESULT 14
S68453
sodium channel protein SNS - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: S68453
R;Akopian, A.N.; Sivilotti, L.; Wood, J.N.
Nature 379, 257-262, 1996
A;Title: A tetrodotoxin-resistant voltage-gated sodium channel expressed by sensory neur
A;Reference number: S68453; MUID:96138382; PMID:8538791
A;Accession: S68453
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1957 <AKO>
A;Cross-references: UNIPROT:Q63554; GB:X92184; NID:g1209466; PIDN:CAA63095.1; PID:g12094
A;Experimental source: dorsal root ganglia
C;Superfamily: sodium channel protein
C;Keywords: sodium channel; transmembrane protein; voltage-gated ion channel
F;132-148/Domain: transmembrane #status predicted <TM1>
F;158-174/Domain: transmembrane #status predicted <TM2>
F;225-241/Domain: transmembrane #status predicted <TM3>
F;249-265/Domain: transmembrane #status predicted <TM4>
F;376-392/Domain: transmembrane #status predicted <TM5>
F;666-682/Domain: transmembrane #status predicted <TM6>
F;702-718/Domain: transmembrane #status predicted <TM7>
F;731-747/Domain: transmembrane #status predicted <TM8>
F;788-804/Domain: transmembrane #status predicted <TM9>

F;865-881/Domain: transmembrane #status predicted <TM10>
F;1156-1172/Domain: transmembrane #status predicted <TM11>
F;1194-1210/Domain: transmembrane #status predicted <TM12>
F;1221-1237/Domain: transmembrane #status predicted <TM13>
F;1286-1302/Domain: transmembrane #status predicted <TM14>
F;1400-1416/Domain: transmembrane #status predicted <TM15>
F;1482-1498/Domain: transmembrane #status predicted <TM16>
F;1516-1532/Domain: transmembrane #status predicted <TM17>
F;1546-1562/Domain: transmembrane #status predicted <TM18>
F;1606-1622/Domain: transmembrane #status predicted <TM19>
F;1708-1724/Domain: transmembrane #status predicted <TM20>

Query Match 46.4%; Score 13; DB 2; Length 1957;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 VVNMYIAVILENF 28
||||||||||||||
Db 1715 VVNMYIAVILENF 1727

RESULT 15
T31340
voltage-gated sodium channel homolog - Bdelloura candida
C;Species: Bdelloura candida
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T31340
R;Jeziorski, M.C.; Greenberg, R.M.; Anderson, P.A.
submitted to the EMBL Data Library, March 1997
A;Description: A putative voltage-gated sodium channel from the turbellarian flatworm Bd
A;Reference number: Z21006
A;Accession: T31340
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1699 <JEZ>
A;Cross-references: UNIPROT:O02037; EMBL:U93074; NID:g1947093; PID:g1947094; PIDN:AAC630
C;Genetics:
A;Gene: Na1
C;Superfamily: sodium channel protein

Query Match 42.9%; Score 12; DB 2; Length 1699;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 VNMYIAVILENF 28
||||||||||||
Db 1536 VNMYIAVILENF 1547

RESULT 16
JC1101
sodium channel protein - Bleeker's squid
C;Species: Loligo bleekeri (Bleeker's squid)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C;Accession: JC1101
R;Sato, C.; Matsumoto, G.
Biochem. Biophys. Res. Commun. 186, 61-68, 1992
A;Title: Primary structure of squid sodium channel deduced from the complementary DNA se
A;Reference number: JC1101; MUID:92337659; PMID:1339273
A;Accession: JC1101
A;Molecule type: mRNA
A;Residues: 1-1522 <SAT>
A;Cross-references: UNIPROT:Q05973; GB:D14525; NID:g287448; PID:g287449
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: phosphoprotein; sodium channel; transmembrane protein; voltage-gated ion cha
F;51-70/Domain: transmembrane #status predicted <TM1>
F;78-100/Domain: transmembrane #status predicted <TM2>
F;113-134/Domain: transmembrane #status predicted <TM3>
F;144-167/Domain: transmembrane #status predicted <TM4>
F;180-201/Domain: transmembrane #status predicted <TM5>
F;309-331/Domain: transmembrane #status predicted <TM6>
F;407-426/Domain: transmembrane #status predicted <TM7>
F;443-464/Domain: transmembrane #status predicted <TM8>
F;473-491/Domain: transmembrane #status predicted <TM9>
F;499-522/Domain: transmembrane #status predicted <TM10>
F;532-553/Domain: transmembrane #status predicted <TM11>
F;605-625/Domain: transmembrane #status predicted <TM12>
F;778-797/Domain: transmembrane #status predicted <TM13>
F;816-837/Domain: transmembrane #status predicted <TM14>
F;847-868/Domain: transmembrane #status predicted <TM15>
F;875-898/Domain: transmembrane #status predicted <TM16>
F;916-937/Domain: transmembrane #status predicted <TM17>
F;1010-1032/Domain: transmembrane #status predicted <TM18>
F;1101-1120/Domain: transmembrane #status predicted <TM19>
F;1133-1154/Domain: transmembrane #status predicted <TM20>
F;1163-1184/Domain: transmembrane #status predicted <TM21>
F;1195-1218/Domain: transmembrane #status predicted <TM22>
F;1237-1258/Domain: transmembrane #status predicted <TM23>
F;1324-1346/Domain: transmembrane #status predicted <TM24>

Query Match 39.3%; Score 11; DB 2; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 NMYIAVILENF 28
||||||||||||
Db 1344 NMYIAVILENF 1354

RESULT 17
JE0084
voltage-gated sodium channel alpha subunit - hydromedusa (Polyorchis penicillatus)
N;Alternate names: PpSCN 1
C;Species: Polyorchis penicillatus
C;Date: 11-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: JE0084
R;Spafford, J.D.; Spencer, A.N.; Gallin, W.J.
Biochem. Biophys. Res. Commun. 244, 772-780, 1998
A;Title: A putative voltage-gated sodium channel alpha subunit (PpSCN1) from the hydrozo
A;Reference number: JE0084; MUID:98205797; PMID:9535741
A;Accession: JE0084
A;Molecule type: mRNA
A;Residues: 1-1695 <SPA>
A;Cross-references: UNIPROT:O62604; GB:AF047380; NID:g3005563; PIDN:AAC38974.1; PID:g300
C;Comment: This protein is the only pore-forming alpha subunit available to account for
C;Superfamily: sodium channel protein
C;Keywords: glycoprotein
F;201,273,299,684,1065,1082,1089,1428/Binding site: carbohydrate (Asn) (covalent) #statu

Query Match 39.3%; Score 11; DB 2; Length 1695;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 NMYIAVILENF 28
||||||||||||
Db 1463 NMYIAVILENF 1473

RESULT 18
A48298
sodium channel homolog - jellyfish (Cyanea capillata)
C;Species: Cyanea capillata
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: A48298
R;Anderson, P.A.V.; Holman, M.A.; Greenberg, R.M.
Proc. Natl. Acad. Sci. U.S.A. 90, 7419-7423, 1993
A;Title: Deduced amino acid sequence of a putative sodium channel from the scyphozoan je
A;Reference number: A48298; MUID:93348284; PMID:8394021
A;Accession: A48298
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1739 <AND>
A;Cross-references: UNIPROT:Q17314; GB:L15445
C;Genetics:
A;Gene: CYNA1
C;Superfamily: sodium channel protein

```
C;Keywords: transmembrane protein

  Query Match             39.3%;  Score 11;  DB 2;  Length 1739;
  Best Local Similarity   100.0%;  Pred. No. 0.0036;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 NMYIAVILENF 28
              ||||||||||
Db       1517 NMYIAVILENF 1527


RESULT 19
T43167
sodium channel protein - California market squid
C;Species: Loligo opalescens (California market squid)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43167
R;Rosenthal, J.J.; Gilly, W.F.
Proc. Natl. Acad. Sci. U.S.A. 90, 10026-10030, 1993
A;Title: Amino acid sequence of a putative sodium channel expressed in the giant axon of
A;Reference number: Z22324; MUID:94052096; PMID:8234251
A;Accession: T43167
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1784 <ROS>
A;Cross-references: UNIPROT:Q25377; EMBL:L19979; NID:g349118; PID:g349119; PIDN:AAA16202
A;Experimental source: stellate ganglia
C;Superfamily: sodium channel protein
C;Keywords: ion transport; membrane protein; sodium channel; voltage-gated ion channel

  Query Match             39.3%;  Score 11;  DB 2;  Length 1784;
  Best Local Similarity   100.0%;  Pred. No. 0.0036;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 NMYIAVILENF 28
              ||||||||||
Db       1582 NMYIAVILENF 1592


RESULT 20
CHEE
sodium channel protein - electric eel
C;Species: Electrophorus electricus (electric eel)
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03178; I50536
R;Noda, M.; Shimizu, S.; Tanabe, T.; Takai, T.; Kayano, T.; Ikeda, T.; Takahashi, H.; Na
da, H.; Miyata, T.; Numa, S.
Nature 312, 121-127, 1984
A;Title: Primary structure of Electrophorus electricus sodium channel deduced from cDNA
A;Reference number: A03178; MUID:85061498; PMID:6209577
A;Accession: A03178
A;Molecule type: mRNA
A;Residues: 1-1820 <NOD>
A;Cross-references: UNIPROT:P02719; GB:X01119; NID:g62776; PIDN:CAA25587.1; PID:g62777
R;Noda, M.; Numa, S.
J. Recept. Res. 7, 467-497, 1987
A;Title: Structure and function of sodium channel.
A;Reference number: I50536; MUID:87311395; PMID:2442385
A;Accession: I50536
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1820 <NO2>
A;Cross-references: GB:M22252; NID:g1041048; PIDN:AAA79960.1; PID:g1041049
C;Comment: This membrane glycoprotein mediates the voltage-dependent sodium-ion permeabi
ss the membrane, the protein forms a sodium-selective channel through which sodium ions
C;Comment: This sequence contains four highly homologous internal repeats (excluding res
 Each repeat has a similar overall structure containing six subregions located in identi
 has a net positive charge (S4), and one is neutral (S2).
C;Comment: The four repeating units are thought to be oriented pseudosymmetrically acros
e. The presence of four homologous structures within this molecule is consistent with th
C;Comment: Available data suggest that activation and inactivation gates are located nea
955 might, in conjunction with the positively charged residues of S4, act as a voltage s
C;Superfamily: sodium channel protein
C;Keywords: duplication; glycoprotein; ion transport; membrane protein; sodium channel;
F;111-419,555-807,989-1281,1311-1587/Region: duplication internal repeats I, II, III and
F;111-141,555-585,989-1019,1311-1341/Region: S1 of repeats I through IV
F;150-171,597-620,1033-1057,1353-1376/Region: S2 of repeats I through IV
F;177-197,626-643,1062-1079,1381-1398/Region: S3 of repeats I through IV
F;204-224,651-671,1092-1112,1417-1437/Region: S4 of repeats I through IV
F;244-264,691-711,1132-1152,1454-1474/Region: S5 of repeats I through IV
F;379-402,767-790,1236-1264,1544-1567/Region: S6 of repeats I through IV
F;205,278,288,317,591,690,797,1160,1174,1806/Binding site: carbohydrate (Asn) (covalent)

  Query Match             39.3%;  Score 11;  DB 1;  Length 1820;
  Best Local Similarity   100.0%;  Pred. No. 0.0037;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 SFLVVVNMYIA 22
              ||||||||||
Db       1554 SFLVVVNMYIA 1564


RESULT 21
A30302
sodium channel protein P15 - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Nov-1997
C;Accession: A30302
R;Ramaswami, M.; Tanouye, M.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 2079-2082, 1989
A;Title: Two sodium-channel genes in Drosophila: implications for channel diversity.
A;Reference number: A30302; MUID:89184571; PMID:2538830
A;Accession: A30302
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-213 <RAM>
C;Genetics:
A;Gene: FlyBase:NaCP60E
A;Cross-references: FlyBase:FBgn0002920
C;Superfamily: sodium channel protein
C;Keywords: duplication

  Query Match             35.7%;  Score 10;  DB 2;  Length 213;
  Best Local Similarity   100.0%;  Pred. No. 0.0065;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 NMYIAVILEN 27
              ||||||||||
Db        171 NMYIAVILEN 180


RESULT 22
S35215
sodium channel protein - house fly
C;Species: Musca domestica (house fly)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S35215
R;Williamson, M.S.; Denholm, I.; Bell, C.A.; Devonshire, A.L.
Mol. Gen. Genet. 240, 17-22, 1993
A;Title: Knockdown resistance (kdr) to DDT and pyrethroid insecticides maps to a sodium
A;Reference number: S35215; MUID:93341454; PMID:8101963
A;Accession: S35215
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-428 <WIL>
A;Cross-references: UNIPROT:Q9TX80
C;Superfamily: sodium channel protein
C;Keywords: duplication

  Query Match             35.7%;  Score 10;  DB 2;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 NMYIAVILEN 27
              ||||||||||
Db        165 NMYIAVILEN 174
```

RESULT 23
S72467
sodium channel protein para-type alpha chain - German cockroach (strain CSMA) (fragment)
C;Species: Blattella germanica (German cockroach)
A;Variety: strain CSMA
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: S72467; S72487
R;Miyazaki, M.; Ohyama, K.; Dunlap, D.Y.; Matsumura, F.
submitted to the EMBL Data Library, September 1996
A;Description: Cloning and sequencing of the para-type sodium channel gene from suscepti
A;Reference number: S72467
A;Accession: S72467
A;Molecule type: mRNA
A;Residues: 1-1689 <MIY>
A;Cross-references: UNIPROT:Q93135; EMBL:U71083; NID:g1633647; PIDN:AAB82037.1; PID:g163
R;Miyazaki, M.; Ohyama, K.; Dunlap, D.Y.; Matsumura, F.
Mol. Gen. Genet. 252, 61-68, 1996
A;Title: Cloning and sequencing of the para-type sodium channel gene from susceptible an
A;Reference number: S72487; MUID:96397510; PMID:8804404
A;Accession: S72487
A;Molecule type: mRNA
A;Residues: 711-819 <MIW>
A;Cross-references: EMBL:U71083
C;Superfamily: sodium channel protein
C;Keywords: duplication; sodium channel; transmembrane protein

  Query Match 35.7%; Score 10; DB 2; Length 1689;
  Best Local Similarity 100.0%; Pred. No. 0.035;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 NMYIAVILEN 27
||||||||||
Db 1614 NMYIAVILEN 1623

RESULT 24
A33299
sodium channel protein - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 21-Nov-1997
C;Accession: A33299
R;Loughney, K.; Kreber, R.; Ganetzky, B.
Cell 58, 1143-1154, 1989
A;Title: Molecular analysis of the para locus, a sodium channel gene in Drosophila.
A;Reference number: A33299; MUID:89376565; PMID:2550145
A;Accession: A33299
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1820 <LOU>
A;Cross-references: GB:M32078; GB:M24285
C;Genetics:
A;Gene: FlyBase:para
A;Cross-references: FlyBase:FBgn0003036
C;Superfamily: sodium channel protein
C;Keywords: duplication; phosphoprotein; transmembrane protein

  Query Match 35.7%; Score 10; DB 2; Length 1820;
  Best Local Similarity 100.0%; Pred. No. 0.038;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 NMYIAVILEN 27
||||||||||
Db 1809 NMYIAVILEN 1818

RESULT 25
S72458
sodium channel protein para-type alpha chain - house fly (strain Cooper)
C;Species: Musca domestica (house fly)
A;Variety: strain Cooper
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
C;Accession: S72458
R;Williamson, M.S.; Martinez-Torres, D.; Hick, C.A.; Devonshire, A.L.
Mol. Gen. Genet. 252, 51-60, 1996
A;Title: Identification of mutations in the housefly para-type sodium channel gene assoc
A;Reference number: S72458; MUID:96397509; PMID:8804403
A;Accession: S72458
A;Molecule type: mRNA
A;Residues: 1-2108 <WIL>
A;Cross-references: UNIPROT:Q94615; EMBL:X96668
A;Experimental source: strain Cooper
C;Genetics:
A;Map position: 3
C;Superfamily: sodium channel protein
C;Keywords: alternative splicing; glycoprotein; phosphoprotein; sodium channel; transmem
F;302,314,332,967,1451,1470/Binding site: carbohydrate (Asn) (covalent) #status predicte
F;541,1208,1582/Binding site: phosphate (Ser) (covalent) #status predicted

  Query Match 35.7%; Score 10; DB 2; Length 2108;
  Best Local Similarity 100.0%; Pred. No. 0.042;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 NMYIAVILEN 27
||||||||||
Db 1841 NMYIAVILEN 1850

Search completed: January 27, 2005, 17:52:48
Job time : 19 secs

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:35:20 ; Search time 92.5 Seconds
(without alignments)
174.167 Million cell updates/sec

Title: US-10-608-584-29
Perfect score: 28
Sequence: 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	100.0	404	2	Q8CCS4	Q8ccs4 mus musculu
2	28	100.0	510	2	Q62242	Q62242 mus musculu
3	28	100.0	519	2	Q9P2J1	Q9p2j1 homo sapien
4	28	100.0	1951	1	CIN3_RAT	P08104 rattus norv
5	28	100.0	1951	2	Q9C007	Q9c007 homo sapien
6	28	100.0	1981	2	Q8IUJ6	Q8iuj6 homo sapien
7	28	100.0	2000	1	CIN3_HUMAN	Q9ny46 homo sapien
8	28	100.0	2005	1	CIN2_HUMAN	Q99250 homo sapien
9	28	100.0	2005	1	CIN2_RAT	P04775 rattus norv
10	28	100.0	2007	2	Q9YGN7	Q9ygn7 cynops pyrr
11	28	100.0	2009	1	CIN1_HUMAN	P35498 homo sapien
12	28	100.0	2009	1	CIN1_RAT	P04774 rattus norv
13	27	96.4	253	2	Q8CAJ8	Q8caj8 mus musculu
14	24	85.7	309	2	Q62205	Q62205 mus musculu
15	24	85.7	1977	2	Q15858	Q15858 homo sapien
16	24	85.7	1984	2	Q28644	Q28644 oryctolagus
17	24	85.7	1984	2	O08562	O08562 rattus norv
18	17	60.7	279	2	O54811	O54811 cavia porce
19	17	60.7	1993	2	P90670	P90670 aplysia cal
20	16	57.1	1880	2	Q9IBF1	Q9ibf1 takifugu pa
21	14	50.0	278	2	O54812	O54812 cavia porce
22	14	50.0	324	2	Q63360	Q63360 rattus norv
23	14	50.0	364	2	Q9P2Q6	Q9p2q6 homo sapien
24	14	50.0	364	2	Q9N2E3	Q9n2e3 pongo pygma
25	14	50.0	364	2	Q9N2E4	Q9n2e4 gorilla gor
26	14	50.0	364	2	Q9N2E5	Q9n2e5 pan troglod
27	14	50.0	1976	2	Q63541	Q63541 rattus norv
28	14	50.0	1978	1	CIN8_MOUSE	Q9wtu3 mus musculu
29	14	50.0	1978	2	O88420	O88420 rattus norv
30	14	50.0	1980	1	CIN8_HUMAN	Q9uqd0 homo sapien
31	14	50.0	1988	2	O88421	O88421 rattus norv
32	13	46.4	523	2	Q62243	Q62243 mus musculu
33	13	46.4	1765	2	O88457	O88457 rattus norv
34	13	46.4	1765	2	Q9JMD4	Q9jmd4 mus musculu
35	13	46.4	1765	2	Q9R053	Q9r053 mus musculu
36	13	46.4	1791	2	Q8NDX3	Q8ndx3 homo sapien
37	13	46.4	1791	2	Q9UHE0	Q9uhe0 homo sapien
38	13	46.4	1791	2	Q9UI33	Q9ui33 homo sapien
39	13	46.4	1956	2	Q9Y5Y9	Q9y5y9 homo sapien
40	13	46.4	1956	2	Q62968	Q62968 rattus norv
41	13	46.4	1957	2	Q6QIY3	Q6qiy3 mus musculu
42	13	46.4	1957	2	Q63554	Q63554 rattus norv
43	13	46.4	1957	2	AAS45602	Aas45602 mus muscu
44	13	46.4	1958	2	P70276	P70276 mus musculu
45	13	46.4	1962	2	O46669	O46669 canis famil
46	12	42.9	46	2	Q71A32	Q71a32 sus scrofa
47	12	42.9	46	2	AAQ11213	Aaq11213 sus scrof
48	12	42.9	1699	2	O02037	O02037 bdelloura c
49	11	39.3	1522	1	CIN1_LOLBL	Q05973 loligo blee
50	11	39.3	1695	2	O62604	O62604 polyorchis
51	11	39.3	1740	2	Q17314	Q17314 cyanea capi
52	11	39.3	1784	2	Q25377	Q25377 loligo opal
53	11	39.3	1820	1	CINA_ELEEL	P02719 electrophor
54	10	35.7	428	2	Q9TX80	Q9tx80 musca domes
55	10	35.7	1089	2	Q8IS97	Q8is97 varroa dest
56	10	35.7	1130	2	Q9XZC1	Q9xzc1 boophilus m
57	10	35.7	1347	2	Q7PMT4	Q7pmt4 anopheles g
58	10	35.7	1361	2	Q7PJH0	Q7pjh0 anopheles g
59	10	35.7	1689	2	Q93135	Q93135 blattella g
60	10	35.7	1695	2	Q94584	Q94584 heliothis v
61	10	35.7	2031	2	O01306	O01306 blattella g
62	10	35.7	2031	2	O01307	O01307 blattella g
63	10	35.7	2051	2	Q86DI7	Q86di7 pediculus h
64	10	35.7	2051	2	Q86DI8	Q86di8 pediculus h
65	10	35.7	2051	2	Q86DI9	Q86di9 pediculus h
66	10	35.7	2058	2	Q6DLT4	Q6dlt4 aedes albop
67	10	35.7	2064	2	Q6DLT3	Q6dlt3 aedes aegyp
68	10	35.7	2086	2	Q86M38	Q86m38 pediculus h
69	10	35.7	2104	2	Q25440	Q25440 musca domes
70	10	35.7	2105	2	Q25439	Q25439 musca domes
71	10	35.7	2108	2	Q94615	Q94615 musca domes
72	10	35.7	2131	1	CINA_DROME	P35500 drosophila
73	10	35.7	2215	2	Q86D77	Q86d77 varroa dest
74	8	28.6	487	2	Q8AV15	Q8av15 gallus gall
75	8	28.6	1834	2	Q28371	Q28371 equus cabal
76	8	28.6	1836	1	CIN4_HUMAN	P35499 homo sapien
77	8	28.6	1840	1	CIN4_RAT	P15390 rattus norv
78	8	28.6	1840	2	O70611	O70611 rattus norv
79	8	28.6	1841	2	Q9ER60	Q9er60 mus musculu
80	7	25.0	79	2	Q9PE09	Q9pe09 xylella fas
81	7	25.0	250	2	Q96YL8	Q96yl8 sulfolobus
82	7	25.0	397	2	Q7ZVG1	Q7zvg1 brachydanio
83	7	25.0	444	2	Q72VU7	Q72vu7 leptospira
84	7	25.0	444	2	Q8F9G4	Q8f9g4 leptospira
85	7	25.0	444	2	AAS68827	Aas68827 leptospir
86	7	25.0	616	2	Q7QWH6	Q7qwh6 giardia lam
87	7	25.0	640	1	PTMA_BUCBP	Q89a36 buchnera ap
88	7	25.0	649	2	Q72SK6	Q72sk6 leptospira
89	7	25.0	649	2	Q8F303	Q8f303 leptospira
90	7	25.0	649	2	AAS69976	Aas69976 leptospir
91	7	25.0	656	2	Q8I260	Q8i260 plasmodium
92	7	25.0	662	2	Q8TU41	Q8tu41 methanosarc
93	7	25.0	675	2	Q9UZ76	Q9uz76 pyrococcus
94	7	25.0	678	2	Q6HCZ6	Q6hcz6 bacillus th
95	7	25.0	678	2	Q81L64	Q81164 bacillus an
96	7	25.0	678	2	AAT33890	Aat33890 bacillus
97	7	25.0	1394	2	Q8H8L9	Q8h819 oryza sativ
98	7	25.0	1717	2	Q90519	Q90519 fugu rubrip
99	7	25.0	1949	2	Q9DF53	Q9df53 brachydanio
100	7	25.0	1962	2	Q75RX9	Q75rx9 homo sapien

ALIGNMENTS

```
RESULT 1
Q8CCS4
ID   Q8CCS4      PRELIMINARY;      PRT;   404 AA.
AC   Q8CCS4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE   enriched library, clone:6430408L10 product:sodium channel protein II
DE   homolog (Fragment).
GN   Name=A230052E19Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AK032187; BAC27748.1; -.
DR   MGD; MGI:2444703; A230052E19Rik.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF00612; IQ; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
FT   NON_TER       1      1
SQ   SEQUENCE   404 AA;  45671 MW;  C5ED26EB0F080C09 CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 404;
  Best Local Similarity   100.0%;  Pred. No. 2e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db        151 GIFFFVSYIIISFLVVVNMYIAVILENF 178


RESULT 2
Q62242
ID   Q62242      PRELIMINARY;      PRT;   510 AA.
AC   Q62242;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Jover E., Shah V.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; L42341; AAA67695.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF00612; IQ; 1.
DR   PRINTS; PR00170; NACHANNEL.
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DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
FT   NON_TER     510    510
SQ   SEQUENCE   510 AA;  58397 MW;  02DCC7DAED3796E8 CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 510;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db        304 GIFFFVSYIIISFLVVVNMYIAVILENF 331


RESULT 3
Q9P2J1
ID   Q9P2J1      PRELIMINARY;      PRT;   519 AA.
AC   Q9P2J1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   KIAA1356 protein (Fragment).
GN   Name=KIAA1356;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20181126; PubMed=10718198;
RA   Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XVI.
RT   The complete sequences of 150 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 7:65-73(2000).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AB037777; BAA92594.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF00612; IQ; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
FT   NON_TER       1      1
SQ   SEQUENCE   519 AA;  58982 MW;  3E8F7ED5E26835FC CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 519;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db        266 GIFFFVSYIIISFLVVVNMYIAVILENF 293


RESULT 4
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CIN3_RAT
ID   CIN3_RAT       STANDARD;      PRT;  1951 AA.
AC   P08104;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Sodium channel protein type III alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.3) (Sodium channel protein, brain III alpha
DE   subunit) (Voltage-gated sodium channel subtype III).
GN   Name=Scn3a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar;
RX   MEDLINE=88137594; PubMed=2449363;
RA   Kayano T., Noda M., Flockerzi V., Takahashi H., Numa S.;
RT   "Primary structure of rat brain sodium channel III deduced from the
RT   cDNA sequence.";
RL   FEBS Lett. 228:187-194(1988).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y00766; CAA68735.1; -.
DR   PIR; S00320; S00320.
DR   PDB; 1QG9; NMR; A=156-176.
DR   RGD; 3635; Scn3a.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; FALSE_NEG.
KW   3D-structure; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   REPEAT      110    455       I.
FT   REPEAT      693    965       II.
FT   REPEAT     1139   1450       III.
FT   REPEAT     1459   1757       IV.
FT   TRANSMEM    124    147       S1 of repeat I.
FT   TRANSMEM    156    175       S2 of repeat I.
FT   TRANSMEM    189    207       S3 of repeat I.
FT   TRANSMEM    214    233       S4 of repeat I.
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FT   TRANSMEM     249     273       S5 of repeat I.
FT   TRANSMEM     401     426       S6 of repeat I.
FT   TRANSMEM     706     730       S1 of repeat II.
FT   TRANSMEM     742     765       S2 of repeat II.
FT   TRANSMEM     774     793       S3 of repeat II.
FT   TRANSMEM     800     820       S4 of repeat II.
FT   TRANSMEM     836     856       S5 of repeat II.
FT   TRANSMEM     910     935       S6 of repeat II.
FT   TRANSMEM    1153    1176       S1 of repeat III.
FT   TRANSMEM    1190    1215       S2 of repeat III.
FT   TRANSMEM    1222    1243       S3 of repeat III.
FT   TRANSMEM    1248    1269       S4 of repeat III.
FT   TRANSMEM    1289    1310       S5 of repeat III.
FT   TRANSMEM    1393    1419       S6 of repeat III.
FT   TRANSMEM    1473    1496       S1 of repeat IV.
FT   TRANSMEM    1508    1531       S2 of repeat IV.
FT   TRANSMEM    1538    1561       S3 of repeat IV.
FT   TRANSMEM    1572    1593       S4 of repeat IV.
FT   TRANSMEM    1609    1631       S5 of repeat IV.
FT   TRANSMEM    1698    1722       S6 of repeat IV.
FT   CARBOHYD     211     211       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     290     290       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     296     296       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     302     302       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     307     307       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     339     339       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     624     624       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     835     835       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1002    1002       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1019    1019       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1085    1085       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1317    1317       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    1331    1331       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   1951 AA;  221385 MW;  74E5E851524BD10E CRC64;

  Query Match             100.0%;  Score 28;  DB 1;  Length 1951;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1698 GIFFFVSYIIISFLVVVNMYIAVILENF 1725


RESULT 5
Q9C007
ID   Q9C007      PRELIMINARY;      PRT;  1951 AA.
AC   Q9C007;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel alpha subunit splice variant SCN3A-
DE   s.
GN   Name=SCN3A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jeong S.-Y., Goto J., Kanazawa I.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AF225986; AAK00218.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1951 AA;  221517 MW;  99AD4C032CE124AB CRC64;

  Query Match             100.0%;  Score 28;  DB 2;  Length 1951;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1698 GIFFFVSYIIISFLVVVNMYIAVILENF 1725


RESULT 6
Q8IUJ6
ID   Q8IUJ6      PRELIMINARY;      PRT;  1981 AA.
AC   Q8IUJ6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel alpha 1 subunit.
GN   Name=SCN1A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Normal brain;
RA   Ouchida M., Ohmori I.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AB098335; BAC45228.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008051; Na_channel1.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   InterPro; IPR000100; Ribonuclease_P.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01664; NACHANNEL1.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS00648; RIBONUCLEASE_P; UNKNOWN_1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1981 AA;  226201 MW;  B1D6946D6491B7AD CRC64;
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  Query Match             100.0%;  Score 28;  DB 2;  Length 1981;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1734 GIFFFVSYIIISFLVVVNMYIAVILENF 1761


RESULT 7
CIN3_HUMAN
ID   CIN3_HUMAN     STANDARD;      PRT;  2000 AA.
AC   Q9NY46; Q16142; Q9BZB3; Q9C006; Q9NYK2; Q9UPD1; Q9Y6P4;
DT   16-OCT-2001 (Rel. 40, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Sodium channel protein type III alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.3) (Sodium channel protein, brain III alpha
DE   subunit) (Voltage-gated sodium channel subtype III).
GN   Name=SCN3A; Synonyms=NAC3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Brain;
RA   Chen Y., Dale T.J., Romanos M.A., Whitaker W.R., Xie X., Clare J.J.;
RT   "Cloning, distribution and functional analysis of the human brain type
RT   III sodium channel from human brain.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RA   Jeong S.-Y., Goto J., Kanazawa I.;
RT   "Cloning of cDNA for human voltage-gated sodium channel alpha subunit,
RT   SCN3A.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND VARIANT THR-606.
RX   MEDLINE=21142400; PubMed=11245985; DOI=10.1016/S0378-1119(00)00594-1;
RA   Kasai N., Fukushima K., Ueki Y., Prasad S., Nosakowski J.,
RA   Sugata K.-I., Sugata A., Nishizaki K., Meyer N.C., Smith R.J.H.;
RT   "Genomic structures of SCN2A and SCN3A - candidate genes for deafness
RT   at the DFNA16 locus.";
RL   Gene 264:113-122(2001).
RN   [4]
RP   SEQUENCE OF 1-1415 FROM N.A. (ISOFORMS 2 AND 4).
RC   TISSUE=Brain;
RX   MEDLINE=98251277; PubMed=9589372;
RA   Lu C.M., Brown G.B.;
RT   "Isolation of a human-brain sodium-channel gene encoding two isoforms
RT   of the subtype III alpha-subunit.";
RL   J. Mol. Neurosci. 10:67-70(1998).
RN   [5]
RP   SEQUENCE OF 1324-1413 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=94211784; PubMed=8159690;
RA   Malo M.S., Srivastava K., Andresen J.M., Chen X.N., Korenberg J.R.,
RA   Ingram V.M.;
RT   "Targeted gene walking by low stringency polymerase chain reaction:
RT   assignment of a putative human brain sodium channel gene (SCN3A) to
RT   chromosome 2q24-31.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:2975-2979(1994).
RN   [6]
RP   SEQUENCE OF 1669-1750 FROM N.A.
RC   TISSUE=Kidney;
RA   Tonkovich G.S., Kyle J.W.;
RT   "Endogenous sodium current in HEK293 cells: increase in cell surface
RT   expression of endogenous currents by stable transfection of the Beta 1
RT   subunit.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC         Comment=Exons 6A and 6N only differ by a single residue;
CC       Name=1; Synonyms=6A-12+12b;
CC         IsoId=Q9NY46-1; Sequence=Displayed;
CC       Name=2; Synonyms=6A-12;
CC         IsoId=Q9NY46-2; Sequence=VSP_001034;
CC       Name=3; Synonyms=6N-12+12b;
CC         IsoId=Q9NY46-3; Sequence=VSP_001033;
CC       Name=4; Synonyms=6N-12;
CC         IsoId=Q9NY46-4; Sequence=VSP_001033, VSP_001034;
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ251507; CAB85895.1; -.
DR   EMBL; AF225987; AAK00219.1; -.
DR   EMBL; AF330135; AAG53414.1; -.
DR   EMBL; AF330118; AAG53414.1; JOINED.
DR   EMBL; AF330119; AAG53414.1; JOINED.
DR   EMBL; AF330120; AAG53414.1; JOINED.
DR   EMBL; AF330121; AAG53414.1; JOINED.
DR   EMBL; AF330122; AAG53414.1; JOINED.
DR   EMBL; AF330123; AAG53414.1; JOINED.
DR   EMBL; AF330124; AAG53414.1; JOINED.
DR   EMBL; AF330125; AAG53414.1; JOINED.
DR   EMBL; AF330126; AAG53414.1; JOINED.
DR   EMBL; AF330127; AAG53414.1; JOINED.
DR   EMBL; AF330128; AAG53414.1; JOINED.
DR   EMBL; AF330129; AAG53414.1; JOINED.
DR   EMBL; AF330130; AAG53414.1; JOINED.
DR   EMBL; AF330131; AAG53414.1; JOINED.
DR   EMBL; AF330132; AAG53414.1; JOINED.
DR   EMBL; AF330133; AAG53414.1; JOINED.
DR   EMBL; AF330134; AAG53414.1; JOINED.
DR   EMBL; AF330135; AAG53415.1; -.
DR   EMBL; AF330118; AAG53415.1; JOINED.
DR   EMBL; AF330119; AAG53415.1; JOINED.
DR   EMBL; AF330120; AAG53415.1; JOINED.
DR   EMBL; AF330121; AAG53415.1; JOINED.
DR   EMBL; AF330122; AAG53415.1; JOINED.
DR   EMBL; AF330123; AAG53415.1; JOINED.
DR   EMBL; AF330124; AAG53415.1; JOINED.
DR   EMBL; AF330125; AAG53415.1; JOINED.
DR   EMBL; AF330126; AAG53415.1; JOINED.
DR   EMBL; AF330127; AAG53415.1; JOINED.
DR   EMBL; AF330128; AAG53415.1; JOINED.
DR   EMBL; AF330129; AAG53415.1; JOINED.
DR   EMBL; AF330130; AAG53415.1; JOINED.
DR   EMBL; AF330131; AAG53415.1; JOINED.
DR   EMBL; AF330132; AAG53415.1; JOINED.
DR   EMBL; AF330133; AAG53415.1; JOINED.
DR   EMBL; AF330134; AAG53415.1; JOINED.
DR   EMBL; AF035685; AAC29514.1; -.
DR   EMBL; AF035686; AAC29515.1; -.
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DR   EMBL; S69887; AAB30530.1; -.
DR   EMBL; AF239921; AAF44690.1; -.
DR   PIR; A54937; A54937.
DR   HSSP; P04775; 1BYY.
DR   Genew; HGNC:10590; SCN3A.
DR   MIM; 182391; -.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; NAS.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; NAS.
DR   GO; GO:0006814; P:sodium ion transport; NAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Polymorphism; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   TRANSMEM    124    147       S1 of repeat I.
FT   TRANSMEM    156    175       S2 of repeat I.
FT   TRANSMEM    189    207       S3 of repeat I.
FT   TRANSMEM    214    233       S4 of repeat I.
FT   TRANSMEM    249    273       S5 of repeat I.
FT   TRANSMEM    401    426       S6 of repeat I.
FT   TRANSMEM    755    779       S1 of repeat II.
FT   TRANSMEM    791    814       S2 of repeat II.
FT   TRANSMEM    823    842       S3 of repeat II.
FT   TRANSMEM    849    869       S4 of repeat II.
FT   TRANSMEM    885    905       S5 of repeat II.
FT   TRANSMEM    959    984       S6 of repeat II.
FT   TRANSMEM   1202   1225       S1 of repeat III.
FT   TRANSMEM   1239   1264       S2 of repeat III.
FT   TRANSMEM   1271   1292       S3 of repeat III.
FT   TRANSMEM   1297   1318       S4 of repeat III.
FT   TRANSMEM   1338   1359       S5 of repeat III.
FT   TRANSMEM   1442   1468       S6 of repeat III.
FT   TRANSMEM   1522   1545       S1 of repeat IV.
FT   TRANSMEM   1557   1580       S2 of repeat IV.
FT   TRANSMEM   1587   1610       S3 of repeat IV.
FT   TRANSMEM   1621   1642       S4 of repeat IV.
FT   TRANSMEM   1658   1680       S5 of repeat IV.
FT   TRANSMEM   1747   1771       S6 of repeat IV.
FT   DOMAIN     1900   1929       IQ.
FT   CARBOHYD    211    211       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    290    290       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    296    296       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    302    302       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    307    307       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    339    339       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    624    624       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    884    884       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1051   1051       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1068   1068       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1134   1134       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1366   1366       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1380   1380       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    208    208       S -> D (in isoform 3 and isoform 4).
FT                                /FTId=VSP_001033.
FT   VARSPLIC    625    673       Missing (in isoform 2 and isoform 4).

  Query Match             100.0%;  Score 28;  DB 1;  Length 2000;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1747 GIFFFVSYIIISFLVVVNMYIAVILENF 1774
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RESULT 8
CIN2_HUMAN
ID   CIN2_HUMAN     STANDARD;      PRT;  2005 AA.
AC   Q99250; Q14472; Q9BZC9; Q9BZD0;
DT   01-JUN-1994 (Rel. 29, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type II alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha
DE   subunit) (HBSC II).
GN   Name=SCN2A; Synonyms=SCN2A2, NAC2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=92390418; PubMed=1325650;
RA   Ahmed C.M., Ware D.H., Lee S.C., Patten C.D., Ferrer-Montiel A.V.,
RA   Schinder A.F., McPherson J.D., Wagner-Mcpherson C.B., Wasmuth J.J.,
RA   Evans G.A., Montal M.;
RT   "Primary structure, chromosomal localization, and functional
RT   expression of a voltage-gated sodium channel from human brain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:8220-8224(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX   MEDLINE=21142400; PubMed=11245985; DOI=10.1016/S0378-1119(00)00594-1;
RA   Kasai N., Fukushima K., Ueki Y., Prasad S., Nosakowski J.,
RA   Sugata K.-I., Sugata A., Nishizaki K., Meyer N.C., Smith R.J.H.;
RT   "Genomic structures of SCN2A and SCN3A - candidate genes for deafness
RT   at the DFNA16 locus.";
RL   Gene 264:113-122(2001).
RN   [3]
RP   SEQUENCE OF 1-89 FROM N.A.
RA   Lu C.-M., Eichelberger J.S., Beckman M.L., Schade S.D., Brown G.B.;
RT   "Isolation of the 5'-flanking region for human brain sodium channel
RT   subtype II alpha-Subunit (SCN2A).";
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1702-2005 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92275082; PubMed=1317301;
RA   Lu C.-M., Han J., Rado T.A., Brown G.B.;
RT   "Differential expression of two sodium channel subtypes in human
RT   brain.";
RL   FEBS Lett. 303:53-58(1992).
RN   [5]
RP   SEQUENCE OF 1702-1772 FROM N.A.
RX   MEDLINE=91110524; PubMed=1846440;
RA   Han J., Lu C.-M., Brown G.B., Rado T.A.;
RT   "Direct amplification of a single dissected chromosomal segment by
RT   polymerase chain reaction: a human brain sodium channel gene is on
RT   chromosome 2q22-q23.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:335-339(1991).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Adult, 6A;
CC         IsoId=Q99250-1; Sequence=Displayed;
CC       Name=2; Synonyms=Neonatal, 6N;
CC         IsoId=Q99250-2; Sequence=VSP_001032;
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
```

```
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M94055; AAA18895.1; -.
DR   EMBL; AF059683; AAC14574.1; -.
DR   EMBL; AF327246; AAG53413.1; -.
DR   EMBL; AF327226; AAG53413.1; JOINED.
DR   EMBL; AF327227; AAG53413.1; JOINED.
DR   EMBL; AF327228; AAG53413.1; JOINED.
DR   EMBL; AF327229; AAG53413.1; JOINED.
DR   EMBL; AF327230; AAG53413.1; JOINED.
DR   EMBL; AF327231; AAG53413.1; JOINED.
DR   EMBL; AF327232; AAG53413.1; JOINED.
DR   EMBL; AF327233; AAG53413.1; JOINED.
DR   EMBL; AF327234; AAG53413.1; JOINED.
DR   EMBL; AF327235; AAG53413.1; JOINED.
DR   EMBL; AF327236; AAG53413.1; JOINED.
DR   EMBL; AF327237; AAG53413.1; JOINED.
DR   EMBL; AF327238; AAG53413.1; JOINED.
DR   EMBL; AF327239; AAG53413.1; JOINED.
DR   EMBL; AF327240; AAG53413.1; JOINED.
DR   EMBL; AF327241; AAG53413.1; JOINED.
DR   EMBL; AF327242; AAG53413.1; JOINED.
DR   EMBL; AF327243; AAG53413.1; JOINED.
DR   EMBL; AF327244; AAG53413.1; JOINED.
DR   EMBL; AF327245; AAG53413.1; JOINED.
DR   EMBL; AF327246; AAG53412.1; -.
DR   EMBL; AF327226; AAG53412.1; JOINED.
DR   EMBL; AF327227; AAG53412.1; JOINED.
DR   EMBL; AF327228; AAG53412.1; JOINED.
DR   EMBL; AF327229; AAG53412.1; JOINED.
DR   EMBL; AF327230; AAG53412.1; JOINED.
DR   EMBL; AF327231; AAG53412.1; JOINED.
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DR   EMBL; AF327233; AAG53412.1; JOINED.
DR   EMBL; AF327234; AAG53412.1; JOINED.
DR   EMBL; AF327235; AAG53412.1; JOINED.
DR   EMBL; AF327236; AAG53412.1; JOINED.
DR   EMBL; AF327237; AAG53412.1; JOINED.
DR   EMBL; AF327238; AAG53412.1; JOINED.
DR   EMBL; AF327239; AAG53412.1; JOINED.
DR   EMBL; AF327240; AAG53412.1; JOINED.
DR   EMBL; AF327241; AAG53412.1; JOINED.
DR   EMBL; AF327242; AAG53412.1; JOINED.
DR   EMBL; AF327243; AAG53412.1; JOINED.
DR   EMBL; AF327244; AAG53412.1; JOINED.
DR   EMBL; AF327245; AAG53412.1; JOINED.
DR   EMBL; X65361; CAA46438.1; ALT_SEQ.
DR   EMBL; M91804; -; NOT_ANNOTATED_CDS.
DR   EMBL; M55662; AAB65854.2; -.
DR   HSSP; P04775; 1BYY.
DR   Genew; HGNC:10588; SCN2A2.
DR   MIM; 601219; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; TAS.
DR   GO; GO:0006814; P:sodium ion transport; TAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   REPEAT      111    456       I.
FT   REPEAT      741   1013       II.
FT   REPEAT     1190   1504       III.
FT   REPEAT     1513   1811       IV.
FT   TRANSMEM    125    148       S1 of repeat I.
FT   TRANSMEM    157    176       S2 of repeat I.
FT   TRANSMEM    190    208       S3 of repeat I.
FT   TRANSMEM    215    234       S4 of repeat I.
FT   TRANSMEM    251    274       S5 of repeat I.
FT   TRANSMEM    402    427       S6 of repeat I.
FT   TRANSMEM    754    778       S1 of repeat II.
FT   TRANSMEM    790    813       S2 of repeat II.
FT   TRANSMEM    822    841       S3 of repeat II.
FT   TRANSMEM    848    867       S4 of repeat II.
FT   TRANSMEM    884    904       S5 of repeat II.
FT   TRANSMEM    958    983       S6 of repeat II.
FT   TRANSMEM   1204   1227       S1 of repeat III.
FT   TRANSMEM   1241   1266       S2 of repeat III.
FT   TRANSMEM   1273   1294       S3 of repeat III.
FT   TRANSMEM   1299   1320       S4 of repeat III.
FT   TRANSMEM   1340   1367       S5 of repeat III.
FT   TRANSMEM   1447   1473       S6 of repeat III.
FT   TRANSMEM   1527   1550       S1 of repeat IV.
FT   TRANSMEM   1562   1585       S2 of repeat IV.
FT   TRANSMEM   1592   1615       S3 of repeat IV.
FT   TRANSMEM   1626   1647       S4 of repeat IV.
FT   TRANSMEM   1663   1685       S5 of repeat IV.
FT   TRANSMEM   1752   1776       S6 of repeat IV.
FT   DOMAIN     1905   1934       IQ.
FT   CARBOHYD    212    212       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    285    285       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    291    291       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    297    297       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    303    303       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    340    340       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    604    604       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    624    624       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    883    883       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1055   1055       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1072   1072       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1136   1136       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1368   1368       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1382   1382       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1393   1393       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1778   1778       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    209    209       D -> N (in isoform 2).
FT                                /FTId=VSP_001032.
FT   CONFLICT    524    524       R -> L (in Ref. 1).

  Query Match             100.0%;  Score 28;  DB 1;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1752 GIFFFVSYIIISFLVVVNMYIAVILENF 1779


RESULT 9
CIN2_RAT
ID   CIN2_RAT       STANDARD;      PRT;  2005 AA.
AC   P04775;
DT   13-AUG-1987 (Rel. 05, Created)
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DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Sodium channel protein type II alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha
DE   subunit).
GN   Name=Scn2a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86146901; PubMed=3754035;
RA   Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M.,
RA   Takahashi H., Numa S.;
RT   "Existence of distinct sodium channel messenger RNAs in rat brain.";
RL   Nature 320:188-192(1986).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X03639; CAA27287.1; -.
DR   PDB; 1BYY; NMR; A=1474-1526.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   3D-structure; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Repeat; Sodium channel; Transmembrane;
KW   Voltage-gated channel.
FT   REPEAT      111    456       I.
FT   REPEAT      741   1013       II.
FT   REPEAT     1190   1504       III.
FT   REPEAT     1513   1811       IV.
FT   TRANSMEM    125    148       S1 of repeat I.
FT   TRANSMEM    157    176       S2 of repeat I.
FT   TRANSMEM    190    208       S3 of repeat I.
FT   TRANSMEM    215    234       S4 of repeat I.
FT   TRANSMEM    251    274       S5 of repeat I.
FT   TRANSMEM    402    427       S6 of repeat I.
FT   TRANSMEM    754    778       S1 of repeat II.
FT   TRANSMEM    790    813       S2 of repeat II.
FT   TRANSMEM    822    841       S3 of repeat II.
FT   TRANSMEM    848    867       S4 of repeat II.
FT   TRANSMEM    884    904       S5 of repeat II.
FT   TRANSMEM    958    983       S6 of repeat II.
FT   TRANSMEM   1204   1227       S1 of repeat III.
FT   TRANSMEM   1241   1266       S2 of repeat III.
FT   TRANSMEM   1273   1294       S3 of repeat III.
FT   TRANSMEM   1299   1320       S4 of repeat III.
FT   TRANSMEM   1340   1367       S5 of repeat III.
FT   TRANSMEM   1447   1473       S6 of repeat III.
FT   TRANSMEM   1527   1550       S1 of repeat IV.
FT   TRANSMEM   1562   1585       S2 of repeat IV.
FT   TRANSMEM   1592   1615       S3 of repeat IV.
FT   TRANSMEM   1626   1647       S4 of repeat IV.
FT   TRANSMEM   1663   1685       S5 of repeat IV.
FT   TRANSMEM   1752   1776       S6 of repeat IV.
FT   DOMAIN     1905   1934       IQ.
FT   CARBOHYD    212    212       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    285    285       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    291    291       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    297    297       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    303    303       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    340    340       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    604    604       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    624    624       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    883    883       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1055   1055       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1072   1072       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1136   1136       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1368   1368       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1382   1382       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1393   1393       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   2005 AA;  227872 MW;  861BE583D79F8324 CRC64;
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Query Match 100.0%; Score 28; DB 1; Length 2005;
Best Local Similarity 100.0%; Pred. No. 6.7e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1752 GIFFFVSYIIISFLVVVNMYIAVILENF 1779
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RESULT 10
Q9YGN7
ID   Q9YGN7      PRELIMINARY;      PRT;  2007 AA.
AC   Q9YGN7;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-dependent sodium channel.
OS   Cynops pyrrhogaster (Japanese common newt).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX   NCBI_TaxID=8330;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RA   Hirota K., Kaneko Y., Matsumoto G., Hanyu Y.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AF123593; AAD17315.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
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DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   2007 AA;  228398 MW;  013E9B9EC9C294C9 CRC64;

  Query Match           100.0%;  Score 28;  DB 2;  Length 2007;
  Best Local Similarity  100.0%;  Pred. No. 6.7e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1754 GIFFFVSYIIISFLVVVNMYIAVILENF 1781


RESULT 11
CIN1_HUMAN
ID   CIN1_HUMAN     STANDARD;      PRT;  2009 AA.
AC   P35498; Q16172; Q96LA3; Q9C008;
DT   01-JUN-1994 (Rel. 29, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type I alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.1) (Sodium channel protein, brain I alpha
DE   subunit).
GN   Name=SCN1A; Synonyms=SCN1, NAC1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS GEFS+2 MET-875 AND
RP   HIS-1648.
RX   MEDLINE=20206553; PubMed=10742094;
RA   Escayg A., MacDonald B.T., Meisler M.H., Baulac S., Huberfeld G.,
RA   An-Gourfinkel I., Brice A., LeGuern E., Moulard B., Chaigne D.,
RA   Buresi C., Malafosse A.;
RT   "Mutations of SCN1A, encoding a neuronal sodium channel, in two
RT   families with GEFS+2.";
RL   Nat. Genet. 24:343-345(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RA   Jeong S.-Y., Goto J., Kanazawa I.;
RT   "Cloning of cDNA for human voltage-gated sodium channel alpha subunit,
RT   SCN1A.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Brain;
RA   Sugawara T., Mazaki E.M., Yamakawa K.;
RT   "Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1)
RT   mRNA.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT THR-1067.
RA   Ouchida M., Ohmori I.;
RT   "Isoforms of human sodium channel SCN1A gene.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 1335-1428 FROM N.A.
RX   MEDLINE=94340991; PubMed=8062593;
RA   Malo M.S., Blanchard B.J., Andresen J.M., Srivastava K., Chen X.N.,
RA   Li X., Jabs E.W., Korenberg J.R., Ingram V.M.;
RT   "Localization of a putative human brain sodium channel gene (SCN1A) to
RT   chromosome band 2q24.";
RL   Cytogenet. Cell Genet. 67:178-186(1994).
RN   [6]
RP   SEQUENCE OF 1518-1940 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92275082; PubMed=1317301;
RA   Lu C.-M., Han J., Rado T.A., Brown G.B.;
RT   "Differential expression of two sodium channel subtypes in human
RT   brain.";
RL   FEBS Lett. 303:53-58(1992).
RN   [7]
RP   VARIANTS GEFS+2 VAL-188; LEU-1353 AND MET-1656.
RX   MEDLINE=21152274; PubMed=11254444;
RA   Wallace R.H., Scheffer I.E., Barnett S., Richards M., Dibbens L.,
RA   Desai R.R., Lerman-Sagie T., Lev D., Mazarib A., Brand N.,
RA   Ben-Zeev B., Goikhman I., Singh R., Kremmidiotis G., Gardner A.,
RA   Sutherland G.R., George A.L. Jr., Mulley J.C., Berkovic S.F.;
RT   "Neuronal sodium-channel alpha1-subunit mutations in generalized
RT   epilepsy with febrile seizures plus.";
RL   Am. J. Hum. Genet. 68:859-865(2001).
RN   [8]
RP   VARIANT GEFS+2 ARG-1204.
RX   MEDLINE=21152275; PubMed=11254445;
RA   Escayg A., Heils A., MacDonald B.T., Haug K., Sander T., Meisler M.H.;
RT   "A novel SCN1A mutation associated with generalized epilepsy with
RT   febrile seizures plus -- and prevalence of variants in patients with
RT   epilepsy.";
RL   Am. J. Hum. Genet. 68:866-873(2001).
RN   [9]
RP   VARIANT SMEI PHE-986.
RX   MEDLINE=21257503; PubMed=11359211;
RA   Claes L., Del-Favero J., Ceulemans B., Lagae L., Van Broeckhoven C.,
RA   De Jonghe P.;
RT   "De novo mutations in the sodium-channel gene SCN1A cause severe
RT   myoclonic epilepsy of infancy.";
RL   Am. J. Hum. Genet. 68:1327-1332(2001).
RN   [10]
RP   VARIANT GEFS+2 THR-1270.
RX   MEDLINE=21630138; PubMed=11756608;
RA   Abou-Khalil B., Ge Q., Desai R., Ryther R., Bazyk A., Bailey R.,
RA   Haines J.L., Sutcliffe J.S., George A.L. Jr.;
RT   "Partial and generalized epilepsy with febrile seizures plus and a
RT   novel SCN1A mutation.";
RL   Neurology 57:2265-2272(2001).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=P35498-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P35498-2; Sequence=VSP_001031;
CC         Note=No experimental confirmation available;
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- DISEASE: Defects in SCN1A are the cause of generalized epilepsy
CC       with febrile seizures plus type 2 (GEFS+2) [MIM:604233]. This
CC       autosomal dominant disorder is characterized by febrile seizures
CC       in children and afebrile seizures in adults. Penetrance is
CC       incomplete and a large intrafamilial variability of the phenotype
CC       is observed.
CC   -!- DISEASE: Defects in SCN1A are a cause of severe myoclonic epilepsy
CC       in infancy (SMEI) [MIM:607208], a severe form of generalized
CC       epilepsy with febrile seizures. SMEI is a rare disorder
CC       characterized by normal development before onset, seizures
CC       beginning in the first year of life in the form of generalized or
CC       unilateral febrile clonic seizures, secondary appearance of
CC       myoclonic seizures, and occasionally partial seizures. It is
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CC       associated with ataxia, slowed psychomotor development, and mental
CC       decline.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF225985; AAK00217.1; -.
DR   EMBL; AY043484; AAK95360.1; -.
DR   EMBL; AB093548; BAC21101.1; -.
DR   EMBL; AB093549; BAC21102.1; -.
DR   EMBL; S71446; AAB31605.1; -.
DR   EMBL; X65362; CAA46439.1; -.
DR   EMBL; M91803; -; NOT_ANNOTATED_CDS.
DR   PIR; I52964; I52964.
DR   PIR; S29184; S29184.
DR   HSSP; P04775; 1BYY.
DR   Genew; HGNC:10585; SCN1A.
DR   MIM; 182389; -.
DR   MIM; 604233; -.
DR   MIM; 607208; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; NAS.
DR   GO; GO:0006814; P:sodium ion transport; NAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008051; Na_channel1.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01664; NACHANNEL1.
DR   PROSITE; PS50096; IQ; FALSE_NEG.
KW   Alternative splicing; Disease mutation; Epilepsy; Glycoprotein;
KW   Ion transport; Ionic channel; Multigene family; Polymorphism; Repeat;
KW   Sodium channel; Transmembrane; Voltage-gated channel.
FT   REPEAT      110    454       I.
FT   REPEAT      750   1022       II.
FT   REPEAT     1200   1514       III.
FT   REPEAT     1523   1821       IV.
FT   TRANSMEM    124    147       S1 of repeat I (By similarity).
FT   TRANSMEM    156    175       S2 of repeat I (By similarity).
FT   TRANSMEM    189    207       S3 of repeat I (By similarity).
FT   TRANSMEM    214    233       S4 of repeat I (By similarity).
FT   TRANSMEM    250    273       S5 of repeat I (By similarity).
FT   TRANSMEM    400    425       S6 of repeat I (By similarity).
FT   TRANSMEM    763    787       S1 of repeat II (By similarity).
FT   TRANSMEM    799    822       S2 of repeat II (By similarity).
FT   TRANSMEM    831    850       S3 of repeat II (By similarity).
FT   TRANSMEM    857    876       S4 of repeat II (By similarity).
FT   TRANSMEM    893    913       S5 of repeat II (By similarity).
FT   TRANSMEM    967    992       S6 of repeat II (By similarity).
FT   TRANSMEM   1214   1237       S1 of repeat III (By similarity).
FT   TRANSMEM   1251   1276       S2 of repeat III (By similarity).
FT   TRANSMEM   1283   1304       S3 of repeat III (By similarity).
FT   TRANSMEM   1309   1330       S4 of repeat III (By similarity).
FT   TRANSMEM   1350   1377       S5 of repeat III (By similarity).
FT   TRANSMEM   1457   1483       S6 of repeat III (By similarity).
FT   TRANSMEM   1537   1560       S1 of repeat IV (By similarity).
FT   TRANSMEM   1572   1595       S2 of repeat IV (By similarity).
FT   TRANSMEM   1602   1625       S3 of repeat IV (By similarity).
FT   TRANSMEM   1636   1657       S4 of repeat IV (By similarity).
FT   TRANSMEM   1673   1695       S5 of repeat IV (By similarity).
FT   TRANSMEM   1762   1786       S6 of repeat IV (By similarity).
FT   CARBOHYD    211    211       N-linked (GlcNAc. . .) (Potential).

  Query Match             100.0%;  Score 28;  DB 1;  Length 2009;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1762 GIFFFVSYIIISFLVVVNMYIAVILENF 1789


RESULT 12
CIN1_RAT
ID   CIN1_RAT       STANDARD;      PRT;  2009 AA.
AC   P04774;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Sodium channel protein type I alpha subunit (Voltage-gated sodium
DE   channel alpha subunit Nav1.1) (Sodium channel protein, brain I alpha
DE   subunit).
GN   Name=Scn1a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86146901; PubMed=3754035;
RA   Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M.,
RA   Takahashi H., Numa S.;
RT   "Existence of distinct sodium channel messenger RNAs in rat brain.";
RL   Nature 320:188-192(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87311395; PubMed=2442385;
RA   Noda M., Numa S.;
RT   "Structure and function of sodium channel.";
RL   J. Recept. Res. 7:467-497(1987).
CC   -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC       of excitable membranes. Assuming opened or closed conformations in
CC       response to the voltage difference across the membrane, the
CC       protein forms a sodium-selective channel through which Na(+) ions
CC       may pass in accordance with their electrochemical gradient.
CC   -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC       3 smaller ones. This sequence represents a large polypeptide.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC       hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC       segment (S4). Segments S4 are probably the voltage-sensors and are
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: Belongs to the sodium channel family.
CC   -!- SIMILARITY: Contains 1 IQ domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X03638; CAA27286.1; -.
DR   EMBL; M22253; AAA79965.1; -.
DR   PIR; A25019; A25019.
DR   HSSP; P04775; 1BYY.
DR   RGD; 69364; Scn1a.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
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DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008051; Na_channel1.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01664; NACHANNEL1.
DR   PROSITE; PS50096; IQ; FALSE_NEG.
KW   Glycoprotein; Ion transport; Ionic channel; Multigene family; Repeat;
KW   Sodium channel; Transmembrane; Voltage-gated channel.
FT   REPEAT      110    454       I.
FT   REPEAT      750   1022       II.
FT   REPEAT     1200   1514       III.
FT   REPEAT     1523   1821       IV.
FT   TRANSMEM    124    147       S1 of repeat I.
FT   TRANSMEM    156    175       S2 of repeat I.
FT   TRANSMEM    189    207       S3 of repeat I.
FT   TRANSMEM    214    233       S4 of repeat I.
FT   TRANSMEM    250    273       S5 of repeat I.
FT   TRANSMEM    400    425       S6 of repeat I.
FT   TRANSMEM    763    787       S1 of repeat II.
FT   TRANSMEM    799    822       S2 of repeat II.
FT   TRANSMEM    831    850       S3 of repeat II.
FT   TRANSMEM    857    876       S4 of repeat II.
FT   TRANSMEM    893    913       S5 of repeat II.
FT   TRANSMEM    967    992       S6 of repeat II.
FT   TRANSMEM   1214   1237       S1 of repeat III.
FT   TRANSMEM   1251   1276       S2 of repeat III.
FT   TRANSMEM   1283   1304       S3 of repeat III.
FT   TRANSMEM   1309   1330       S4 of repeat III.
FT   TRANSMEM   1350   1377       S5 of repeat III.
FT   TRANSMEM   1457   1483       S6 of repeat III.
FT   TRANSMEM   1537   1560       S1 of repeat IV.
FT   TRANSMEM   1572   1595       S2 of repeat IV.
FT   TRANSMEM   1602   1625       S3 of repeat IV.
FT   TRANSMEM   1636   1657       S4 of repeat IV.
FT   TRANSMEM   1673   1695       S5 of repeat IV.
FT   TRANSMEM   1762   1786       S6 of repeat IV.
FT   CARBOHYD    211    211       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    284    284       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    295    295       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    301    301       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    306    306       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    338    338       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    601    601       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    621    621       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    681    681       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    892    892       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1060   1060       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1064   1064       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1080   1080       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1146   1146       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1378   1378       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1392   1392       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1403   1403       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   2009 AA;  228769 MW;  6808466F6368373B CRC64;

  Query Match           100.0%;  Score 28;  DB 1;  Length 2009;
  Best Local Similarity  100.0%;  Pred. No. 6.7e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1762 GIFFFVSYIIISFLVVVNMYIAVILENF 1789


RESULT 13
Q8CAJ8
ID   Q8CAJ8      PRELIMINARY;      PRT;   253 AA.
AC   Q8CAJ8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched
DE   library, clone:A230052E19 product:sodium channel protein II homolog
DE   (Fragment).
GN   Name=A230052E19Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK038645; BAC30078.1; -.
DR   MGD; MGI:2444703; A230052E19Rik.
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DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR001696; Na_channel.
DR   Pfam; PF00612; IQ; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ionic channel.
FT   NON_TER       1      1
SQ   SEQUENCE   253 AA;  29041 MW;  B6B1C4CC35AE571E CRC64;

  Query Match             96.4%;  Score 27;  DB 2;  Length 253;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-18;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 IFFFVSYIIISFLVVVNMYIAVILENF 28
              |||||||||||||||||||||||||||
Db          1 IFFFVSYIIISFLVVVNMYIAVILENF 27


RESULT 14
Q62205
ID   Q62205      PRELIMINARY;      PRT;   309 AA.
AC   Q62205;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Sodium channel 25.
GN   Name=Scn9a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Jover E., Shah V.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; L42338; AAA67106.1; -.
DR   MGD; MGI:107636; Scn9a.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF00612; IQ; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   309 AA;  34971 MW;  975165758B88D3EC CRC64;

  Query Match             85.7%;  Score 24;  DB 2;  Length 309;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-15;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db         63 FVSYIIISFLVVVNMYIAVILENF 86


RESULT 15
Q15858
ID   Q15858      PRELIMINARY;      PRT;  1977 AA.
AC   Q15858;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel alpha subunit.
GN   Name=hNE-Na;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thyroid;
RX   MEDLINE=95237189; PubMed=7720699;
RA   Klugbauer N., Lacinova L., Flockerzi V., Hofmann F.;
RT   "Structure and functional expression of a new member of the
RT   tetrodotoxin-sensitive voltage-activated sodium channel family from
RT   human neuroendocrine cells.";
RL   EMBO J. 14:1084-1090(1995).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; X82835; CAA58042.1; -.
DR   PIR; S54771; S54771.
DR   HSSP; P04775; 1BYY.
DR   Genew; HGNC:10597; SCN9A.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; TAS.
DR   GO; GO:0006814; P:sodium ion transport; TAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1977 AA;  225195 MW;  17D67CBC32BC15FB CRC64;

  Query Match             85.7%;  Score 24;  DB 2;  Length 1977;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-15;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1729 FVSYIIISFLVVVNMYIAVILENF 1752


RESULT 16
Q28644
ID   Q28644      PRELIMINARY;      PRT;  1984 AA.
AC   Q28644;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel alpha-subunit.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=New Zealand White; TISSUE=Sciatic nerve;
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RX   MEDLINE=96074641; PubMed=7479931;
RA   Belcher S.M., Zerillo C.A., Levenson R., Ritchie J.M., Howe J.R.;
RT   "Cloning of a sodium channel alpha subunit from rabbit Schwann
RT   cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:11034-11038(1995).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; U35238; AAA89159.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1984 AA;  225748 MW;  98F76860C9866AA0 CRC64;

  Query Match             85.7%;  Score 24;  DB 2;  Length 1984;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-15;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1737 FVSYIIISFLVVVNMYIAVILENF 1760


RESULT 17
O08562
ID   O08562      PRELIMINARY;      PRT;  1984 AA.
AC   O08562;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   PN1 (Voltage-gated sodium channel) (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97188502; PubMed=9037087;
RA   Toledo-Aral J.J., Moss B.L., He Z.J., Koszowski A.G., Whisenand T.,
RA   Levinson S.R., Wolf J.J., Silos-Santiago I., Halegoua S., Mandel G.;
RT   "Identification of PN1, a predominant voltage-dependent sodium channel
RT   expressed principally in peripheral neurons.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:1527-1532(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97007982; PubMed=8854872;
RA   Kozak C.A., Sangameswaran L.;
RT   "Genetic mapping of the peripheral sodium channel genes, Scn9a and
RT   Scn10a, in the mouse.";
RL   Mamm. Genome 7:787-788(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Sangameswaran L., Fish L.M., Koch B.D., Rabert D.K., Delgado S.G.,
RA   Ilnicka M., Jakeman L.B., Novakovic S., Wong K., Sze P., Tzoumaka E.,
RA   Stewart G.R., Herman R.C., Chan H., Eglen R.M., Hunter J.C.;
RT   "A novel tetrodotoxin-sensitive, voltage-gated sodium channel
RT   expressed in rat and human dorsal root ganglia.";
RL   J. Biol. Chem. 0:0-0(1997).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; U79568; AAB50403.1; -.
DR   EMBL; AF000368; AAB80701.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
FT   NON_TER    1984    1984
SQ   SEQUENCE   1984 AA;  226037 MW;  386C38B9B5097091 CRC64;

  Query Match             85.7%;  Score 24;  DB 2;  Length 1984;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-15;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1738 FVSYIIISFLVVVNMYIAVILENF 1761


RESULT 18
O54811
ID   O54811      PRELIMINARY;      PRT;  279 AA.
AC   O54811;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   GPBI (Fragment).
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebellum;
RX   MEDLINE=97338144; PubMed=9192691;
RA   de Miera E.V.S., Rudy B., Sugimori M., Llinas R.;
RT   "Molecular characterization of the sodium channel subunits expressed
RT   in mammalian cerebellar Purkinje cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:7059-7064(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebellum;
RA   Vega-Saenz de Miera E., Rudy B., Sugimori M., Llinos R.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF003372; AAC02899.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR005821; Ion_trans.
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DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR00169; KCHANNEL.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER     279    279
SQ   SEQUENCE   279 AA;  31625 MW;  1504A333CA63DD24 CRC64;

  Query Match             60.7%;  Score 17;  DB 2;  Length 279;
  Best Local Similarity   100.0%;  Pred. No. 1e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFPFVSYIIISFLVVV 17
              |||||||||||||||||
Db        263 GIFPFVSYIIISFLVVV 279


RESULT 19
P90670
ID   P90670      PRELIMINARY;      PRT;  1993 AA.
AC   P90670;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sodium channel alpha-subunit SCAP1.
OS   Aplysia californica (California sea hare).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC   Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC   Aplysioidea; Aplysiidae; Aplysia.
OX   NCBI_TaxID=6500;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Nervous system;
RX   MEDLINE=97238630; PubMed=9115644;
RA   Dyer J.R., Johnston W.L., Castellucci V.F., Dunn R.J.;
RT   "Cloning and tissue distribution of the Aplysia Na+ channel alpha-
RT   subunit cDNA.";
RL   DNA Cell Biol. 16:347-356(1997).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; U66915; AAC47457.1; -.
DR   PIR; T30902; T30902.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1993 AA;  225896 MW;  33E174B9BF07E1A7 CRC64;

  Query Match             60.7%;  Score 17;  DB 2;  Length 1993;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 SFLVVVNMYIAVILENF 28
              |||||||||||||||||
Db       1719 SFLVVVNMYIAVILENF 1735


RESULT 20
Q9IBF1
ID   Q9IBF1      PRELIMINARY;      PRT;  1880 AA.
AC   Q9IBF1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel.
OS   Takifugu pardalis (Panther puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=98921;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=20090650; PubMed=10623632;
RA   Yotsu-Yamashita M., Nishimori K., Nitanai Y., Isemura M., Sugimoto A.,
RA   Yasumoto T.;
RT   "Binding properties of 3H-PbTx-3 and 3H-saxitoxin to brain membranes
RT   and to skeletal muscle membranes of puffer fish Fugu pardalis, and the
RT   primary structure of a voltage-gated Na+ channel alpha-subunit (fMNa1)
RT   from skeletal muscle of F. pardalis.";
RL   Biochem. Biophys. Res. Commun. 267:403-412(2000).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AB030482; BAA90398.1; -.
DR   HSSP; P04775; 1BYY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
SQ   SEQUENCE   1880 AA;  212084 MW;  406483C6C3D43E02 CRC64;

  Query Match             57.1%;  Score 16;  DB 2;  Length 1880;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 SYIIISFLVVVNMYIA 22
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Db       1608 SYIIISFLVVVNMYIA 1623


RESULT 21
O54812
ID   O54812      PRELIMINARY;      PRT;   278 AA.
AC   O54812;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   CerIII (Fragment).
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebellum;
```

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RX   MEDLINE=97338144; PubMed=9192691;
RA   de Miera E.V.S., Rudy B., Sugimori M., Llinas R.;
RT   "Molecular characterization of the sodium channel subunits expressed
RT   in mammalian cerebellar Purkinje cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:7059-7064(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebellum;
RA   Vega-Saenz de Miera E., Rudy B., Sugimori M., Llinos R.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF003373; AAC02900.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR00169; KCHANNEL.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER     278    278
SQ   SEQUENCE   278 AA;  31866 MW;  65741B14C6AE649A CRC64;

  Query Match             50.0%;  Score 14;  DB 2;  Length 278;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFL 14
              ||||||||||||||
Db        262 GIFFFVSYIIISFL 275


RESULT 22
Q63360
ID   Q63360      PRELIMINARY;      PRT;   324 AA.
AC   Q63360;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Na+ channel (Fragment).
GN   Name=Na+ channel;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Myocardium;
RX   MEDLINE=89292178; PubMed=2544627;
RA   Sills M.N., Xu Y.C., Baracchini E., Goodman R.H., Cooperman S.S.,
RA   Mandel G., Chien K.R.;
RT   "Expression of diverse Na+ channel messenger RNAs in rat myocardium:
RT   Evidence for a cardiac-specific Na+ channel.";
RL   J. Clin. Invest. 84:331-336(1989).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; M27223; AAA41666.1; -.
DR   PIR; A45752; A45752.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF00612; IQ; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
FT   NON_TER       1      1
SQ   SEQUENCE   324 AA;  36863 MW;  95CBE148E354E198 CRC64;

  Query Match             50.0%;  Score 14;  DB 2;  Length 324;
  Best Local Similarity   100.0%;  Pred. No. 1e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFL 14
              ||||||||||||||
Db         86 GIFFFVSYIIISFL 99


RESULT 23
Q9P2Q6
ID   Q9P2Q6      PRELIMINARY;      PRT;   364 AA.
AC   Q9P2Q6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Voltage-gated sodium channel alpha subunit (Fragment).
GN   Name=SCN8A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kitano T., Kobayakawa H., Saitou N.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AB037525; BAA90445.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF00612; IQ; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
FT   NON_TER       1      1
FT   NON_TER     364    364
SQ   SEQUENCE   364 AA;  41263 MW;  BA5760C962BE6786 CRC64;

  Query Match             50.0%;  Score 14;  DB 2;  Length 364;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFL 14
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Db        131 GIFFFVSYIIISFL 144


RESULT 24
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Q9N2E3
ID   Q9N2E3      PRELIMINARY;      PRT;   364 AA.
AC   Q9N2E3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Voltage-gated sodium channel alpha subunit (Fragment).
GN   Name=SCN8A;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kitano T., Kobayakawa H., Saitou N.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AB037528; BAA90448.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF00612; IQ; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
FT   NON_TER       1      1
FT   NON_TER     364    364
SQ   SEQUENCE   364 AA;  41235 MW;  975760C962BE6791 CRC64;

  Query Match             50.0%;  Score 14;  DB 2;  Length 364;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFL 14
              ||||||||||||||
Db        131 GIFFFVSYIIISFL 144


RESULT 25
Q9N2E4
ID   Q9N2E4      PRELIMINARY;      PRT;   364 AA.
AC   Q9N2E4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Voltage-gated sodium channel alpha subunit (Fragment).
GN   Name=SCN8A;
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kitano T., Kobayakawa H., Saitou N.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AB037527; BAA90447.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006814; P:sodium ion transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF00612; IQ; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW   Transport; Voltage-gated channel.
FT   NON_TER       1      1
FT   NON_TER     364    364
SQ   SEQUENCE   364 AA;  41263 MW;  BA5760C962BE6786 CRC64;

  Query Match             50.0%;  Score 14;  DB 2;  Length 364;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFL 14
              ||||||||||||||
Db        131 GIFFFVSYIIISFL 144


Search completed: January 27, 2005, 17:51:35
Job time : 94.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:36:50 ; Search time 22.5 Seconds
(without alignments)
82.529 Million cell updates/sec

Title: US-10-608-584-29
Perfect score: 28
Sequence: 1 GIFFFVSYIIISFLVVVNMYIAVILENF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	100.0	310	3	US-08-605-284B-13	Sequence 13, Appl
2	28	100.0	310	3	US-08-605-284B-14	Sequence 14, Appl
3	28	100.0	310	3	US-08-605-284B-15	Sequence 15, Appl
4	28	100.0	2005	3	US-08-836-325-7	Sequence 7, Appli
5	28	100.0	2005	4	US-09-457-571-7	Sequence 7, Appli
6	27	96.4	309	3	US-08-605-284B-4	Sequence 4, Appli
7	27	96.4	309	3	US-08-605-284B-5	Sequence 5, Appli
8	25	89.3	813	3	US-08-836-325-8	Sequence 8, Appli
9	25	89.3	813	4	US-09-457-571-8	Sequence 8, Appli
10	24	85.7	1011	3	US-08-836-325-2	Sequence 2, Appli
11	24	85.7	1011	4	US-09-457-571-2	Sequence 2, Appli
12	24	85.7	1835	3	US-08-836-325-15	Sequence 15, Appl
13	24	85.7	1835	4	US-09-457-571-15	Sequence 15, Appl
14	24	85.7	1969	3	US-08-836-325-16	Sequence 16, Appl
15	24	85.7	1969	4	US-09-457-571-16	Sequence 16, Appl
16	24	85.7	1977	4	US-09-976-594-757	Sequence 757, App
17	24	85.7	1977	4	US-09-919-039-367	Sequence 367, App
18	24	85.7	1984	3	US-08-836-325-10	Sequence 10, Appl
19	24	85.7	1984	4	US-09-457-571-10	Sequence 10, Appl
20	24	85.7	1989	3	US-08-836-325-11	Sequence 11, Appl
21	24	85.7	1989	3	US-08-836-325-12	Sequence 12, Appl
22	24	85.7	1989	4	US-09-457-571-11	Sequence 11, Appl
23	24	85.7	1989	4	US-09-457-571-12	Sequence 12, Appl
24	17	60.7	310	3	US-08-605-284B-16	Sequence 16, Appl
25	16	57.1	310	3	US-08-605-284B-10	Sequence 10, Appl
26	14	50.0	232	3	US-09-024-020B-6	Sequence 6, Appli
27	14	50.0	232	3	US-09-425-043-6	Sequence 6, Appli
28	14	50.0	309	3	US-08-605-284B-6	Sequence 6, Appli
29	14	50.0	1976	3	US-09-024-020B-9	Sequence 9, Appli
30	14	50.0	1976	3	US-09-425-043-9	Sequence 9, Appli
31	14	50.0	1978	3	US-09-024-020B-3	Sequence 3, Appli
32	14	50.0	1978	3	US-09-425-043-3	Sequence 3, Appli
33	14	50.0	1988	3	US-09-024-020B-4	Sequence 4, Appli
34	14	50.0	1988	3	US-09-425-043-4	Sequence 4, Appli
35	13	46.4	311	3	US-08-605-284B-23	Sequence 23, Appl
36	13	46.4	521	4	US-08-669-656A-4	Sequence 4, Appli
37	13	46.4	1765	4	US-09-354-147C-2	Sequence 2, Appli
38	13	46.4	1765	4	US-09-354-147C-3	Sequence 3, Appli
39	13	46.4	1765	4	US-09-354-147C-5	Sequence 5, Appli
40	13	46.4	1791	4	US-09-354-147C-42	Sequence 42, Appl
41	13	46.4	1956	3	US-08-843-417-2	Sequence 2, Appli
42	13	46.4	1956	3	US-08-843-417-10	Sequence 10, Appl
43	13	46.4	1956	4	US-09-527-013-2	Sequence 2, Appli
44	13	46.4	1956	4	US-09-527-013-10	Sequence 10, Appl
45	13	46.4	1957	4	US-08-669-656A-2	Sequence 2, Appli
46	13	46.4	1957	4	US-08-669-656A-8	Sequence 8, Appli
47	13	46.4	2132	4	US-08-669-656A-6	Sequence 6, Appli
48	11	39.3	311	3	US-08-605-284B-18	Sequence 18, Appl
49	11	39.3	312	3	US-08-605-284B-20	Sequence 20, Appl
50	11	39.3	317	3	US-08-605-284B-17	Sequence 17, Appl
51	10	35.7	307	3	US-08-605-284B-19	Sequence 19, Appl
52	10	35.7	413	2	US-08-808-793-25	Sequence 25, Appl
53	10	35.7	452	3	US-07-998-289B-6	Sequence 6, Appli
54	10	35.7	1820	3	US-07-998-289B-8	Sequence 8, Appli
55	10	35.7	2100	2	US-08-808-793-23	Sequence 23, Appl
56	10	35.7	2100	3	US-08-772-512A-19	Sequence 19, Appl
57	10	35.7	2104	2	US-08-808-793-4	Sequence 4, Appli
58	10	35.7	2104	3	US-08-772-512A-4	Sequence 4, Appli
59	10	35.7	2105	2	US-08-808-793-3	Sequence 3, Appli
60	10	35.7	2105	3	US-08-772-512A-3	Sequence 3, Appli
61	8	28.6	310	3	US-08-605-284B-12	Sequence 12, Appl
62	8	28.6	1836	4	US-10-162-012-24	Sequence 24, Appl
63	7	25.0	24	2	US-08-295-643-4	Sequence 4, Appli
64	7	25.0	24	3	US-08-473-265-3	Sequence 3, Appli
65	7	25.0	24	3	US-08-284-747-3	Sequence 3, Appli
66	7	25.0	309	3	US-08-605-284B-11	Sequence 11, Appl
67	7	25.0	2016	3	US-09-634-920-4	Sequence 4, Appli
68	7	25.0	2016	4	US-09-514-907A-2	Sequence 2, Appli
69	7	25.0	2016	4	US-09-896-994-2	Sequence 2, Appli
70	7	25.0	2016	4	US-09-840-125-4	Sequence 4, Appli
71	6	21.4	64	4	US-09-248-796A-23205	Sequence 23205, A
72	6	21.4	77	4	US-09-513-999C-7113	Sequence 7113, Ap
73	6	21.4	84	4	US-09-270-767-32717	Sequence 32717, A
74	6	21.4	84	4	US-09-270-767-47934	Sequence 47934, A
75	6	21.4	103	4	US-09-710-279-1708	Sequence 1708, Ap
76	6	21.4	103	4	US-09-710-279-2074	Sequence 2074, Ap
77	6	21.4	110	4	US-09-248-796A-21277	Sequence 21277, A
78	6	21.4	120	4	US-09-252-991A-26987	Sequence 26987, A
79	6	21.4	127	4	US-09-583-110-4717	Sequence 4717, Ap
80	6	21.4	167	4	US-09-270-767-37083	Sequence 37083, A
81	6	21.4	167	4	US-09-270-767-52300	Sequence 52300, A
82	6	21.4	170	3	US-09-393-245-4	Sequence 4, Appli
83	6	21.4	171	4	US-09-134-000C-5689	Sequence 5689, Ap
84	6	21.4	176	4	US-09-248-796A-18892	Sequence 18892, A
85	6	21.4	195	4	US-09-107-532A-3898	Sequence 3898, Ap
86	6	21.4	196	3	US-09-134-001C-4286	Sequence 4286, Ap
87	6	21.4	204	4	US-09-270-767-56679	Sequence 56679, A
88	6	21.4	210	4	US-09-270-767-39769	Sequence 39769, A
89	6	21.4	210	4	US-09-270-767-54986	Sequence 54986, A
90	6	21.4	230	4	US-09-328-352-7370	Sequence 7370, Ap
91	6	21.4	232	4	US-09-107-532A-5235	Sequence 5235, Ap
92	6	21.4	246	4	US-09-583-110-4242	Sequence 4242, Ap
93	6	21.4	273	4	US-09-396-149-12	Sequence 12, Appl
94	6	21.4	273	4	US-09-396-149-14	Sequence 14, Appl
95	6	21.4	273	4	US-09-396-149-16	Sequence 16, Appl
96	6	21.4	273	4	US-09-396-149-20	Sequence 20, Appl
97	6	21.4	273	4	US-09-396-149-22	Sequence 22, Appl
98	6	21.4	300	4	US-09-393-634-62	Sequence 62, Appl
99	6	21.4	316	4	US-09-583-110-4475	Sequence 4475, Ap
100	6	21.4	318	4	US-09-396-149-18	Sequence 18, Appl

ALIGNMENTS

```
RESULT 1
US-08-605-284B-13
; Sequence 13, Application US/08605284B
; Patent No. 6060271
;  GENERAL INFORMATION:
;    APPLICANT:  WALEWSKI, JOSE L.
;    APPLICANT:  RECIO-PINTO, ESPERANZA
;    TITLE OF INVENTION:  VOLTAGE GATED SODIUM CHANNELS FROM
;    TITLE OF INVENTION:  HUMAN PERIPHERAL NERVE
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;      STREET:  CLINTON SQUARE, P.O. BOX 1051
;      CITY:  ROCHESTER
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/605,284B
;      FILING DATE:  09-FEB-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BRAMAN, SUSAN J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/800 (CRF D-1705)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  716-263-1636
;      TELEFAX:  716-263-1600
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  310 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-605-284B-13

  Query Match             100.0%;  Score 28;  DB 3;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-21;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db        283 GIFFFVSYIIISFLVVVNMYIAVILENF 310


RESULT 2
US-08-605-284B-14
; Sequence 14, Application US/08605284B
; Patent No. 6060271
;  GENERAL INFORMATION:
;    APPLICANT:  WALEWSKI, JOSE L.
;    APPLICANT:  RECIO-PINTO, ESPERANZA
;    TITLE OF INVENTION:  VOLTAGE GATED SODIUM CHANNELS FROM
;    TITLE OF INVENTION:  HUMAN PERIPHERAL NERVE
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;      STREET:  CLINTON SQUARE, P.O. BOX 1051
;      CITY:  ROCHESTER
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/605,284B
;      FILING DATE:  09-FEB-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BRAMAN, SUSAN J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/800 (CRF D-1705)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  716-263-1636
;      TELEFAX:  716-263-1600
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  310 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-605-284B-14

  Query Match             100.0%;  Score 28;  DB 3;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-21;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db        283 GIFFFVSYIIISFLVVVNMYIAVILENF 310


RESULT 3
US-08-605-284B-15
; Sequence 15, Application US/08605284B
; Patent No. 6060271
;  GENERAL INFORMATION:
;    APPLICANT:  WALEWSKI, JOSE L.
;    APPLICANT:  RECIO-PINTO, ESPERANZA
;    TITLE OF INVENTION:  VOLTAGE GATED SODIUM CHANNELS FROM
;    TITLE OF INVENTION:  HUMAN PERIPHERAL NERVE
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;      STREET:  CLINTON SQUARE, P.O. BOX 1051
;      CITY:  ROCHESTER
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/605,284B
;      FILING DATE:  09-FEB-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BRAMAN, SUSAN J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/800 (CRF D-1705)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  716-263-1636
;      TELEFAX:  716-263-1600
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  310 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  protein
US-08-605-284B-15

  Query Match             100.0%;  Score 28;  DB 3;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-21;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db        283 GIFFFVSYIIISFLVVVNMYIAVILENF 310


RESULT 4
US-08-836-325-7
; Sequence 7, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2005 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-836-325-7

  Query Match             100.0%;  Score 28;  DB 3;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1752 GIFFFVSYIIISFLVVVNMYIAVILENF 1779


RESULT 5
US-09-457-571-7
; Sequence 7, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2005 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-457-571-7

  Query Match             100.0%;  Score 28;  DB 4;  Length 2005;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||||||
Db       1752 GIFFFVSYIIISFLVVVNMYIAVILENF 1779


RESULT 6
US-08-605-284B-4
; Sequence 4, Application US/08605284B
; Patent No. 6060271
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  WALEWSKI, JOSE L.
;    APPLICANT:  RECIO-PINTO, ESPERANZA
;    TITLE OF INVENTION:  VOLTAGE GATED SODIUM CHANNELS FROM
;    TITLE OF INVENTION:  HUMAN PERIPHERAL NERVE
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;      STREET:  CLINTON SQUARE, P.O. BOX 1051
;      CITY:  ROCHESTER
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/605,284B
;      FILING DATE:  09-FEB-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BRAMAN, SUSAN J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/800 (CRF D-1705)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  716-263-1636
;      TELEFAX:  716-263-1600
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  309 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-605-284B-4

  Query Match                 96.4%;  Score 27;  DB 3;  Length 309;
  Best Local Similarity  100.0%;  Pred. No. 5.3e-20;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILEN 27
              |||||||||||||||||||||||||||
Db        283 GIFFFVSYIIISFLVVVNMYIAVILEN 309


RESULT 7
US-08-605-284B-5
; Sequence 5, Application US/08605284B
; Patent No. 6060271
;  GENERAL INFORMATION:
;    APPLICANT:  WALEWSKI, JOSE L.
;    APPLICANT:  RECIO-PINTO, ESPERANZA
;    TITLE OF INVENTION:  VOLTAGE GATED SODIUM CHANNELS FROM
;    TITLE OF INVENTION:  HUMAN PERIPHERAL NERVE
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;      STREET:  CLINTON SQUARE, P.O. BOX 1051
;      CITY:  ROCHESTER
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/605,284B
;      FILING DATE:  09-FEB-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BRAMAN, SUSAN J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/800 (CRF D-1705)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  716-263-1636
;      TELEFAX:  716-263-1600
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  309 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-605-284B-5

  Query Match                 96.4%;  Score 27;  DB 3;  Length 309;
  Best Local Similarity  100.0%;  Pred. No. 5.3e-20;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVVVNMYIAVILEN 27
              |||||||||||||||||||||||||||
Db        283 GIFFFVSYIIISFLVVVNMYIAVILEN 309


RESULT 8
US-08-836-325-8
; Sequence 8, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  813 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-836-325-8

  Query Match             89.3%;  Score 25;  DB 3;  Length 813;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 FFVSYIIISFLVVVNMYIAVILENF 28
              |||||||||||||||||||||||||
Db        617 FFVSYIIISFLVVVNMYIAVILENF 641


RESULT 9
US-09-457-571-8
; Sequence 8, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  813 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-457-571-8

  Query Match             89.3%;  Score 25;  DB 4;  Length 813;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-17;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 FFVSYIIISFLVVVNMYIAVILENF 28
              |||||||||||||||||||||||||
Db        617 FFVSYIIISFLVVVNMYIAVILENF 641


RESULT 10
US-08-836-325-2
; Sequence 2, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1011 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-836-325-2

  Query Match             85.7%;  Score 24;  DB 3;  Length 1011;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db        785 FVSYIIISFLVVVNMYIAVILENF 808


RESULT 11
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US-09-457-571-2
; Sequence 2, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1011 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-457-571-2

  Query Match             85.7%;  Score 24;  DB 4;  Length 1011;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db        785 FVSYIIISFLVVVNMYIAVILENF 808


RESULT 12
US-08-836-325-15
; Sequence 15, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1835 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-836-325-15

  Query Match             85.7%;  Score 24;  DB 3;  Length 1835;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1604 FVSYIIISFLVVVNMYIAVILENF 1627


RESULT 13
US-09-457-571-15
; Sequence 15, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
```

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;       COUNTRY:  USA
;       ZIP:  20005-3934
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/457,571
;       FILING DATE:  09-DEC-1999
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/836,325
;       FILING DATE:  02-MAY-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/14251
;       FILING DATE:  02-NOV-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/482,401
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/334,029
;       FILING DATE:  02-NOV-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ludwig, Steven R.
;       REGISTRATION NUMBER:  36,203
;       REFERENCE/DOCKET NUMBER:  0917.0240003
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  15:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1835 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  protein
US-09-457-571-15

  Query Match             85.7%;  Score 24;  DB 4;  Length 1835;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1604 FVSYIIISFLVVVNMYIAVILENF 1627


RESULT 14
US-08-836-325-16
; Sequence 16, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;     APPLICANT:  Mandel, Gail
;     APPLICANT:  Halegoua, Simon
;     APPLICANT:  Borden, Laurence A.
;     TITLE OF INVENTION:  Peripheral Nervous System Specific
;     TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;     TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;     TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;     TITLE OF INVENTION:  Thereof
;     NUMBER OF SEQUENCES:  19
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;       STREET:  1100 New York Ave., N. W., Suite 600
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20005-3934
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/836,325
;       FILING DATE:  2-MAY-1997
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/14251
;       FILING DATE:  02-NOV-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/482,401
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/334,029
;       FILING DATE:  02-NOV-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ludwig, Steven R.
;       REGISTRATION NUMBER:  36,203
;       REFERENCE/DOCKET NUMBER:  0917.0240002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  16:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1969 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-836-325-16

  Query Match             85.7%;  Score 24;  DB 3;  Length 1969;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1721 FVSYIIISFLVVVNMYIAVILENF 1744


RESULT 15
US-09-457-571-16
; Sequence 16, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;     APPLICANT:  Mandel, Gail
;     APPLICANT:  Halegoua, Simon
;     TITLE OF INVENTION:  Peripheral Nervous System Specific
;     TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;     TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;     TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;     TITLE OF INVENTION:  Thereof
;     NUMBER OF SEQUENCES:  19
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;       STREET:  1100 New York Ave., N. W., Suite 600
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20005-3934
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/457,571
;       FILING DATE:  09-DEC-1999
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/836,325
;       FILING DATE:  02-MAY-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/14251
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;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1969 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-457-571-16

  Query Match             85.7%;  Score 24;  DB 4;  Length 1969;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1721 FVSYIIISFLVVVNMYIAVILENF 1744


RESULT 16
US-09-976-594-757
; Sequence 757, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 757
;   LENGTH: 1977
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 1719478CD1
US-09-976-594-757

  Query Match             85.7%;  Score 24;  DB 4;  Length 1977;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1729 FVSYIIISFLVVVNMYIAVILENF 1752


RESULT 17
US-09-919-039-367
; Sequence 367, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
;  APPLICANT: Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;  FILE REFERENCE: PA-0035 US
;  CURRENT APPLICATION NUMBER: US/09/919,039
;  CURRENT FILING DATE:  2002-09-09
;  PRIOR APPLICATION NUMBER: 60/222,113
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 401
;  SOFTWARE: PERL Program
; SEQ ID NO 367
;   LENGTH: 1977
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6727066 1719478CD1
US-09-919-039-367

  Query Match             85.7%;  Score 24;  DB 4;  Length 1977;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1729 FVSYIIISFLVVVNMYIAVILENF 1752


RESULT 18
US-08-836-325-10
; Sequence 10, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1984 amino acids
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;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-836-325-10

  Query Match             85.7%;  Score 24;  DB 3;  Length 1984;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1738 FVSYIIISFLVVVNMYIAVILENF 1761


RESULT 19
US-09-457-571-10
; Sequence 10, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1984 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-457-571-10

  Query Match             85.7%;  Score 24;  DB 4;  Length 1984;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1738 FVSYIIISFLVVVNMYIAVILENF 1761


RESULT 20
US-08-836-325-11
; Sequence 11, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1989 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-836-325-11

  Query Match             85.7%;  Score 24;  DB 3;  Length 1989;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1740 FVSYIIISFLVVVNMYIAVILENF 1763


RESULT 21
US-08-836-325-12
; Sequence 12, Application US/08836325
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; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1989 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-836-325-12

  Query Match             85.7%;  Score 24;  DB 3;  Length 1989;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1740 FVSYIIISFLVVVNMYIAVILENF 1763


RESULT 22
US-09-457-571-11
; Sequence 11, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/457,571
;      FILING DATE:  09-DEC-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,325
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1989 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-09-457-571-11

  Query Match             85.7%;  Score 24;  DB 4;  Length 1989;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1740 FVSYIIISFLVVVNMYIAVILENF 1763


RESULT 23
US-09-457-571-12
; Sequence 12, Application US/09457571
; Patent No. 6703486
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
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;       ZIP:  20005-3934
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/457,571
;       FILING DATE:  09-DEC-1999
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/836,325
;       FILING DATE:  02-MAY-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/14251
;       FILING DATE:  02-NOV-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/482,401
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/334,029
;       FILING DATE:  02-NOV-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ludwig, Steven R.
;       REGISTRATION NUMBER:  36,203
;       REFERENCE/DOCKET NUMBER:  0917.0240003
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1989 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  protein
US-09-457-571-12

  Query Match             85.7%;  Score 24;  DB 4;  Length 1989;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 FVSYIIISFLVVVNMYIAVILENF 28
              ||||||||||||||||||||||||
Db       1740 FVSYIIISFLVVVNMYIAVILENF 1763


RESULT 24
US-08-605-284B-16
; Sequence 16, Application US/08605284B
; Patent No. 6060271
;  GENERAL INFORMATION:
;     APPLICANT:  WALEWSKI, JOSE L.
;     APPLICANT:  RECIO-PINTO, ESPERANZA
;     TITLE OF INVENTION:  VOLTAGE GATED SODIUM CHANNELS FROM
;     TITLE OF INVENTION:  HUMAN PERIPHERAL NERVE
;     NUMBER OF SEQUENCES:  23
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;       STREET:  CLINTON SQUARE, P.O. BOX 1051
;       CITY:  ROCHESTER
;       STATE:  NEW YORK
;       COUNTRY:  USA
;       ZIP:  14603
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/605,284B
;       FILING DATE:  09-FEB-1996
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BRAMAN, SUSAN J.
;       REGISTRATION NUMBER:  34,103
;       REFERENCE/DOCKET NUMBER:  19603/800 (CRF D-1705)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  716-263-1636
;       TELEFAX:  716-263-1600
;   INFORMATION FOR SEQ ID NO:  16:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  310 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-605-284B-16

  Query Match             60.7%;  Score 17;  DB 3;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-10;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 SFLVVVNMYIAVILENF 28
              |||||||||||||||||
Db        294 SFLVVVNMYIAVILENF 310


RESULT 25
US-08-605-284B-10
; Sequence 10, Application US/08605284B
; Patent No. 6060271
;  GENERAL INFORMATION:
;     APPLICANT:  WALEWSKI, JOSE L.
;     APPLICANT:  RECIO-PINTO, ESPERANZA
;     TITLE OF INVENTION:  VOLTAGE GATED SODIUM CHANNELS FROM
;     TITLE OF INVENTION:  HUMAN PERIPHERAL NERVE
;     NUMBER OF SEQUENCES:  23
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;       STREET:  CLINTON SQUARE, P.O. BOX 1051
;       CITY:  ROCHESTER
;       STATE:  NEW YORK
;       COUNTRY:  USA
;       ZIP:  14603
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/605,284B
;       FILING DATE:  09-FEB-1996
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BRAMAN, SUSAN J.
;       REGISTRATION NUMBER:  34,103
;       REFERENCE/DOCKET NUMBER:  19603/800 (CRF D-1705)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  716-263-1636
;       TELEFAX:  716-263-1600
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  310 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-605-284B-10

  Query Match             57.1%;  Score 16;  DB 3;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-09;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIFFFVSYIIISFLVV 16
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Db 283 GIFFFVSYIIISFLVV 298

Search completed: January 27, 2005, 17:54:20
Job time : 23.5 secs